gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca   1153
Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr
            370   375   380

gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa   1201
Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys
            385   390   395

cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata   1249
Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile
        400   405   410

ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc   1297
Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro
415   420   425   430

cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg   1345
Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met
                435   440   445

gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc   1393
Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile
            450   455   460

tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag   1441
Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln
            465   470   475

cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag   1489
Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu
            480   485   490

aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc   1537
Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

351/527

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         495                   500                   505                   510
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc     1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser
                   515                   520                   525
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga     1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg
                   530                   535                   540
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg     1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg
              545                   550                   555
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg     1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val
         560                   565                   570
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc     1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys
575                   580                   585                   590
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc     1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr
                   595                   600                   605
gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc     1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly
                   610                   615                   620
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga     1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly
              625                   630                   635
gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttccct    1975
Glu Lys Tyr Ile Asp Leu Arg His
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640   645

gcctggacca ttcccagctc cctgctcact cttctctcag ccaaagctca aagggactag 2035

agagaagcct cctgctcccc tcgcctgcac accccctttc agagggccac tgggttagga 2095

cctgaggacc tcacttggcc ctgcaaggcc cgcttttcag ggaccagtcc accaccatct 2155

cctccacgtt gagtgaagct catcccaagc aaggagcccc agtctcccga gcgggtagga 2215

gagtttcttg cagaacgtgt tttttcttta cacacattat gctgtaaata cgctcgtcct 2275

gccagcagct gagctgggta gcctctctga gctggtttcc tgccccaaag gctggcattc 2335

caccatccag gtgcaccact gaagtgagga cacaccggag ccaggcgcct gctcatgttg 2395

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cacaaagtca gacgagacca tcctggctaa cacggtgaaa ccctgtctct actaaaaata 2695

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gaagcaggag aatggtatga atccaggagg tggagcttgc agtgagccga gaccgtgcca 2815

ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaa aaatcgtgct 2875

cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935

tcccatagcc ctcttgatgg atcacgtaaa actgaaaggc agcggggagc agacaaagat 2995

gaggtctaca ctgtccttca tggggattaa agctatggtt atattagcac caaacttcta 3055

caaaccaagc tcaggaccca accctagaag ggcccaaatg agagaatggt acttagggat 3115

ggcaaaacgg gcctggctag agcttcgggt gtgtgtgtct gtctgtgtat gcatacatat 3175

gtgtgtatat atggttttgt caggtgtgta aatttgcaaa ttgtttcctt tatatatgta 3235

tgtatatata tatatgaaaa tatatatata tatgaaaaat aaagcttaat tgtcccag   3293

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<211> 646

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<400> 96

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Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
                20   25   30

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
            35   40   45

Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
        50   55   60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
65   70   75   80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
                85   90   95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
            100   105   110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
        115   120   125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
        130   135   140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
145   150   155   160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
                165   170   175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
        180   185   190

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
        195   200   205

Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
        210   215   220

Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
225   230   235   240

Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
                445   250   255

Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
                260   265   270

Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
        275   280   285

Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
        290   295   300

Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
305   310   315   320

Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
                325   330   335

Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
                340   345   350

Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
                355   360   365

Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
        370   375   380

Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
385   390   395   400

Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

                405   410   415
Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp

           420   425   430
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu

      435   440   445
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp

   450   455   460
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val

465   470   475   480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly

                485   490   495
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu

           500   505   510
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr

           515   520   525
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn

      530   535   540
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val

545   550   555   560
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly

           565   570   575
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg

           580   585   590
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu

      595   600   605
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu

            610   615   620

Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys

625   630   635   640

Tyr Ile Asp Leu Arg His

                    645

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ggggaccagc agctgtcgcc gccgctctca gggtgaagag ggaacagaaa tctttgcccc 120

ctgactttgg aaatctcgtt taaccttcaa actggcg atg tca agg gtt cca agt 175

                                        Met Ser Arg Val Pro Ser
                                          1   5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223
Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp
              10   15   20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271
Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile
          25   30   35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319
Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

                    40   45   50

tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga   367
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg
     55   60   65   70

gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt   415
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu
                    75   80   85

tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc   463
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe
                    90   95   100

aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag   511
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu
               105   110   115

agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag   559
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys
               120   125   130

aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc   607
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu
135   140   145   150

cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat   655
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp
                    155   160   165

tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct   703
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro
               170   175   180

gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg   751
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg

358/527

        185   190   195

ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac   799

Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His

        200   205   210

aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa   847

Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu

215   220   225   230

cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg   895

His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val

            235   240   245

gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag   943

Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys

         250   255   260

gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac   991

Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp

        265   270   275

aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc   1039

Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys

      280   285   290

agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac   1087

Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp

295   300   305   310

ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac   1135

Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn

         315   320   325

tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg   1183

                    Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val
                              330   335   340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca   1231
Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser
          345   350   355

gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc   1279
Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser
          360   365   370

taagatcctg cttgttgtaa gactccgttt aatttccaga agcagcagcc actgttgctg   1339

ccactgacca ccaggtagac agcgcaatct gtggagcttt tactctgttg tgaggggaag   1399

agactgcatt gtggccccag actttttaaaa cagcactaaa taacttgggg gaaacggggg   1459

gagggaaaat gaaatgaaaa ccctgttgct gcgtcactgt gttccctttg gcctgtctga   1519

gtttgatact gtggggattc agtttaggcg ctggcccgag gatatcccag cggtggtact   1579

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agg   1642

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<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

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            20   25   30

Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met
        35   40   45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
      50   55   60

Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
 65   70   75   80

Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
                      85   90   95

Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
                 100   105   110

Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
             115   120   125

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
     130   135   140

Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
145   150   155   160

Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
                 165   170   175

Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
             180   185   190

Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
             195   200   205

Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
     210   215   220

Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
225   230   235   240

Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
             245   250   255

Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

                 260   265   270

Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met

            275   280   285

Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu

         290   295   300

Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln

305   310   315   320

Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser

                 325   330   335

Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala

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            355   360   365

Lys Arg Leu Lys Gln Ser

      370

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<211> 5722

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<220>

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                                                          Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc   165
Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr
          5   10   15

aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt   213
Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe
         20   25   30

gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag   261
Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys
     35   40   45   50

ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg   309
Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu
                  55   60   65

atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg   357
Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val
                 70   75   80

cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag   405
Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys
              85   90   95

aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc   453
Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly
         100   105   110

cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc   501
Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu
115   120   125   130

agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct   549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala

          135   140   145

ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtg cag gaa   597

Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu

          150   155   160

gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag   645

Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu

          165   170   175

ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc   693

Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile

          180   185   190

gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg   741

Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly

195   200   205   210

gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc   789

Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile

                  215   220   225

ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt   837

Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu Thr Leu

                230   235   240

gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac   885

Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr

          245   250   255

att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt   933

Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys

          260   265   270

gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att   981

Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile
275   280   285   290

gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa   1029
Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys
                    295   300   305

gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga   1077
Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly
                310   315   320

gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag   1125
Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu
            325   330   335

tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc   1173
Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro
        340   345   350

atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct   1221
Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro
355   360   365   370

cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc   1269
Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser
                    375   380   385

gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc   1317
Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg
                390   395   400

ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tcg gtc   1365
Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val
            405   410   415

cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag   1413
Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln
        420   425   430

gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca   1461
Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
435   440   445   450

tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc   1509
Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
                    455   460   465

ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa   1557
Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
                410   475   480

gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg   1605
Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp
            485   490   495

tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa   1653
Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys
        500   505   510

cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac   1701
Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp
515   520   525   530

tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt   1749
Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys
            535   540   545

cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt   1797
Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys
            550   555   560

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act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt   1845
Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly
        565                 570                 575

tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa   1893
Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu
        580                 585                 590

gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac   1941
Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn
595                 600                 605                 610

acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc   1989
Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly
        615                 620                 625

tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag   2037
Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln
        630                 635                 640

gtg tgc aag ccc cgt aac ccc tgc acg gat ggg acc cac gac tgc aac   2085
Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn
        645                 650                 655

aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac   2133
Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr
        660                 665                 670

cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg   2181
Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly
675                 680                 685                 690

gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg   2229
Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val
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                    695   700   705

gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc   2277
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro

            710   715   720

aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt   2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys

        725   730   735

gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt   2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys

        740   745   750

cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg   2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val

755   760   765   770

gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca   2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala

                775   780   785

gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat   2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp

            790   795   800

gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat   2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn

            805   810   815

gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac   2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp

        820   825   830

aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac   2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp

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     835                840                845                850
cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc    2709
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly
                   855                860                865
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag    2757
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln
              870                875                880
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat    2805
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp
         885                890                895
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc    2853
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro
    900                905                910
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc    2901
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys
915                920                925                930
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt    2949
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys
                   935                940                945
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg    2997
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met
              950                955                960
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt    3045
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val
         965                970                975
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct    3093
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Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro

      980   985   990

gga ctc gct gta ggt tat gat gag ttt aat gct gtg gac ttc agt ggc   3141

Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly

995   1000   1005   1010

acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc   3189

Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val

            1015   1020   1025

ttt ggc tac cag tcc agc agc cgc ttt tat gtt gtg atg tgg aag caa   3237

Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln

         1030   1035   1040

gtc acc cag tcc tac tgg gac acc aac ccc acg agg gct cag gga tac   3285

Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr

       1045   1050   1055

tcg ggc ctt tct gtg aaa gtt gta aac tcc acc aca ggg cct ggc gag   3333

Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu

      1060   1065   1070

cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg   3381

His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val

1075   1080   1085   1090

cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc   3429

Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr

          1095   1100   1105

gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga   3477

Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg

       1110   1115   1120

gtg gtg atg tat gaa ggg aag aaa atc atg gct gac tca gga ccc atc   3525

Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile

      1125   1130   1135

tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct   3573

Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser

   1140   1145   1150

caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc   3621

Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro

1155   1160   1165   1170

taatcatcaa attgttgatt gaaagactga tcataaacca atgctggtat tgcaccttct 3681

ggaactatgg gcttgagaaa accccagga tcacttctcc ttggcttcct tcttttctgt 3741

gcttgcatca gtgtggactc ctagaacgtg cgacctgcct caagaaaatg cagttttcaa 3801

aaacagactc atcagcattc agcctccaat gaataagaca tcttccaagc atataaacaa 3861

ttgctttggt ttccttttga aaaagcatct acttgcttca gttgggaagg tgcccattcc 3921

actctgcctt tgtcacagag cagggtgcta ttgtgaggcc atctctgagc agtggactca 3981

aaagcatttt caggcatgtc agagaaggga ggactcacta gaattagcaa acaaaaccac 4041

cctgacatcc tccttcagga acacggggag cagaggccaa agcactaagg ggagggcgca 4101

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gacttcctcc ctgatcccca cccttactca tcaccttgca gtggccagaa ttagggaatc 4341

agaatcaaac cagtgtaagg cagtgctggc tgccattgcc tggtcacatt gaaattggtg 4401

gcttcattct agatgtagct tgtgcagatg tagcaggaaa ataggaaaac ctaccatctc 4461

agtgagcacc agctgcctcc caaaggaggg gcagccgtgc ttatattttt atggttacaa 4521

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cagtctaata agctgctctg ccccttgtgc tcagagtgga tgttatggga ttcctttttt 4941

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caaagaaagc catgaggtct tcaatactgt tttaccccat cccttgtgca tatttccagg 5061

gagaaggaaa gcatatacac ttttttcttt catttttcca aaagagaaaa aaatgacaaa 5121

aggtgaaact tacatacaaa tattacctca tttgttgtgt gactgagtaa agaattttg 5181

gatcaagcgg aaagagttta agtgtctaac aaacttaaag ctactgtagt acctaaaaag 5241

tcagtgttgt acatagcata aaaactctgc agagaagtat tcccaataag gaaatagcat 5301

tgaaatgtta aatacaattt ctgaaagtta tgtttttttt ctatcatctg gtataccatt 5361

gctttatttt tataaattat tttctcattg ccattggaat agaatattca gattgtgtag 5421

atatgctatt taaataattt atcaggaaat actgcctgta gagttagtat ttctattttt 5481

atataatgtt tgcacactga attgaagaat tgttggtttt ttcttttttt tgtttttttt 5541

tttttttttt ttttttttgc ttttgacctc ccattttttac tatttgccaa tacctttttc 5601

taggaatgtg ctttttttttg tacacattt tatccatttt acattctaaa gcagtgtaag 5661

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<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
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Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp

                    20   25   30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu

               35   40   45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala

               50   55   60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp

          65   70   75   80

Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln

                         85   90   95

Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His

               100   105   110

Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu

               115   120   125

Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu

          130   135   140

Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val

     145   150   155   160

Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn

                    165   170   175

Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala

               180   185   190

Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe

               195   200   205

Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu

          210   215   220

Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu

     225   230   235   240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
           245   250   255

Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
           260   265   270

Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
           275   280   285

Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
           290   295   300

Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
305   310   315   320

Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
           325   330   335

Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
           340   345   350

Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
           355   360   365

Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
           370   375   380

Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
385   390   395   400

Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
           405   410   415

Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
           420   425   430

Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
           435   440   445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
    450   455   460

Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465   470   475   480

Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
        485   490   495

Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
     500   505   510

Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly
      515   520   525

Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
    530   535   540

Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
545   550   555   560

Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
       565   570   575

Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
      580   585   590

Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
     595   600   605

Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
    610   615   620

Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
625   630   635   640

Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
    645   650   655

Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

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                660                    665                    670
  Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile
                675                    680                    685
  Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val
            690                    695                    700
  Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn
  705                    710                    715                    720
  Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp
                    725                    730                    735
  Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp
                740                    745                    750
  Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp
                755                    760                    765
  Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp
            770                    775                    780
  Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp
  785                    790                    795                    800
  Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val
                    805                    810                    815
  Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln
                820                    825                    830
  Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp
            835                    840                    845
  Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu
            850                    855                    860
  Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala
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                865   870   875   880

Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His

                    885   890   895

Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu

            900   905   910

Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp

                915   920   925

Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp

            930   935   940

Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe

945   950   955   960

Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn

                965   970   975

Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys

                980   985   990

Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe

            995   1000   1005

Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly

            1010   1015   1020

Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp

1025   1030   1035   1040

Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln

                1045   1050   1055

Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro

            1060   1065   1070

Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly

            1075   1080   1085

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

  1090   1095   1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105   1110   1115   1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

    1125   1130   1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

    1140   1145   1150

Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

   1155   1160   1165

Asp Pro

  1170

<210> 101

<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35)..(568)

<400> 101

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                 Met Ser Gly Gly Lys Tyr Val

                 1   5

gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

   10   15   20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag   151
Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys
          25   30   35

caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac   199
Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp
  40   45   50   55

cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg   247
Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val
                  60   65   70

att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc   295
Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala
                  75   80   85

agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg   343
Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu
                  90   95   100

tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc   391
Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe
          105   110   115

gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag   439
Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys
120   125   130   135

agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac   487
Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr
                  140   145   150

gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc   535
Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe

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                155                  160                  165
agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588
Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile

                170                  175
gaagtatacc tgattttttt tcctttttaat tttcctggtg ccaatttcaa gttccaagtt 648
gctaatacag caacgaattt atgaattgaa ttatcttggt tgaaaataaa aagatcactt 708
tctcagtttt cataagtatt atgtctcttc tgagctattt catctatttt tggcagtctg 768
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<210> 102

<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

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Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met
                20                  25                  30

Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu
            35                  40                  45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val
        50                  55                  60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser
65                  70                  75                  80

Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys
                85                  90                  95
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Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala
              100   105   110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp
              115   120   125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr
              130   135   140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe
145   150   155   160

Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys
                  165   170   175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(444)

<400> 103

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 1   5   10   15

ctg ttc ctc acc atc cct ttc gcc ttc ttc ctg ccc gag ctg ata ttt   96
Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe
              20   25   30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc   144

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      Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro
                  35                  40                  45

      ttg ctg caa gga tgg gtg atg tat gtc tcg ctc acc tcg ttt ctc atc    192
      Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile
                  50                  55                  60

      tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt    240
      Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe
            65                  70                  75                  80

      gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc    288
      Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile
                        85                  90                  95

      ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct    336
      Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser
                  100                 105                 110

      gag aaa ctg ctg gac cca aga att tac tac att aat tcg gca gcc tcg    384
      Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser
                  115                 120                 125

      ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc    432
      Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser
                  130                 135                 140

      atc tat tac cac tgatgcacag gcgccaggcc aagggggaaa tgctctttga        484
      Ile Tyr Tyr His
      145

      aagctccaat tattggtccc caaaagcagc ttccaacgtt tgccatctgg atgacaaacg    544

      gaagatccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca    604

      ccacactttg tttggacatt taaattcact ctgctgaata ggaggaagct tttctttttc    664

      ctgggaaaac aactgtctct tggaattatc tgaccatgaa cttgctcttc tagacaactc    724
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acatcaaagc cctcactcca ctaatggaga atcctagccc cactaatgcc aagtctgttt 784

ggggattttg cctcagctat gggcttccct agagtaggtc taggggaata ctcagtctga 844

tctttttttt gtttgtttta ttttgttttt tttgagacgg agtctcgctc ttcctccaag 904

gctggagtgc agtgacgcga tctccactca ctgcaggctc cgcctcccgg gttcccgcca 964

ttctcctgcc tcagcctccc gagtagccgg gactacaggc gcccaccacc atgcccggct 1024

aatttagttg tatttttagt agagatgggg tttcaccgta ttagccagga tggtctcgat 1084

ctcctgacct cgtgatccgc ccgcctcggc ctcccaaagt gctgggatta caggcgtgag 1144

ccaccgtgcc cggcctgatt ctcttaaaat tgaagaggtg ctgccaaggc cttcagatct 1204

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gctgccggac gcctgggtca ggaatccaag accccacctc ttaaggactg gttcctcaga 1564

aagcaccctc agggaaaaag gtgaaaacat tacatccgtg gattctcctg ccacaaccgc 1624

attggaagaa aaggctgccg caacatctca gcgaggagtg aaggacccat gtcccaggaa 1684

ccgcgctgcg ccacctgcac tcacccccct cacattctct taagcacccg gtggccctcc 1744

gaggctggcg gaatggtggt gcccacgggg ttgggcaagg gctcaccagg acctcaacgg 1804

gcaaagttgt gcacactaaa atatcaaatc aaggtgcttg gttttaaagt aaatgttttt 1864

ctaaagaaag ctgtgttctt ctgttgaccc agacgaatag ggcacagccc tgtaactgca 1924

cgtgccttct gtcattggga atgaaataaa ttattacgag aaagggactt gtcctaactg 1984

gtttgaggcc ttacagtttt gtatctacat ttttcccctc ctggggtttg cggggacagg 2044

gacagaacta caggagtcat gggaaagaaa attctggctt cactactgct cactgctcac 2104

tttctgatca ctctgatact ttttttttttt tttttttttt gcaacctgat accttgaaaa 2164

gcttctatgt gtctctcctt ttgttgcctg gcagctgtct aggatgatca ctgattacta 2224

tttactaagt agccacatgc aaataaaagt tgtttggtaa aatgg   2269

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<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

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1   5   10   15

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     20   25   30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

     35   40   45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

     50   55   60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65   70   75   80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

     85   90   95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

     100   105   110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

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     130   135   140

Ile Tyr Tyr His

145

<210> 105

<211> 2899

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<221> CDS

<222> (91)..(2196)

<400> 105

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gggcctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114
                                    Met Ala Ala Pro Met Thr Pro Ala
                                    1   5

gct cgg ccc gag gac tac gag gcg gcg ctc aat gcc gcc ctg gct gac 162
Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp
        10   15   20

gtg ccc gaa ctg gcc aga ctc ctg gag atc gac ccg tac ttg aag ccc 210
Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro
25   30   35   40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258
Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu
                45   50   55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306
Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly
                60   65   70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354
Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser
        75   80   85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt   402
Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe
        90   95   100

aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga   450
Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly
105   110   115   120

aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg   498
Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val
                125   130   135

cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag   546
Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu
                140   145   150

atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt   594
Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly
        155   160   165

gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat   642
Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr
        170   175   180

gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat   690
Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr
185   190   195   200

gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat   738
Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr
                205   210   215

aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac   786
Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr
                220   225   230

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc   834
Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser
            235   240   245

ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga   882
Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly
            250   255   260

aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt   930
Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly
265   270   275   280

atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca   978
Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser
            285   290   295

gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat   1026
Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His
            300   305   310

tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc   1074
Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala
            315   320   325

tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg   1122
Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp
            330   335   340

tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg   1170
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
345   350   355   360

tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat   1218
Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp

387/527

                  365   370   375

tac agt gaa tat ttc gga cta caa gta gat gaa gat gcc ttg act tac   1266
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr

             380   385   390

ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata   1314
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile

          395   400   405

aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att   1362
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile

        410   415   420

tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca   1410
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro

425   430   435   440

gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac   1458
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn

             445   450   455

atg ggc gat ata gta tac acg ctc aca aac agg cgc tac ctt gaa aag   1506
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys

             460   465   470

tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag   1554
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys

          475   480   485

tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt   1602
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser

        490   495   500

gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat   1650
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His

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      505                  510                  515                  520
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc    1698
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu

                    525                  530                  535
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca    1746
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro

               540                  545                  550
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat    1794
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His

          555                  560                  565
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac    1842
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp

     570                  575                  580
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca    1890
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro

585                  590                  595                  600
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt    1938
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe

                    605                  610                  615
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc    1986
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser

               620                  625                  630
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att    2034
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile

          635                  640                  645
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac    2082
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Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp
        650   655   660

cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc   2130

His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro
665   670   675   680

tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag   2178

Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln
                 685   690   695

aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat   2226

Asn Val Asp Leu Pro Asn
            700

gcagatttgt gttttgtttt cttgttatca ctgtcacaca gcttataaca tgtatgcttt 2286

tcagaataca gttgtctagc caagccatca agtgtctgaa attcaatatt ggtttatgca 2346

aatacagcaa acttttattt aagtagatag gagaatatgt ttaaaatatt aggaatccta 2406

gaccatattt tcaagtcatc ttagcagcta ggattctcaa atggaagtgt tatatataat 2466

atgttaaaaa cattttgctt tcctggctaa ttatttgatc cttttaaatc caaatttgaa 2526

tcatttgtca tgtatgatta tttctgttaa atgtacacag tatttaagat ggatatttgg 2586

tggctctatt tgttctgata tcttttggtc taaattatga ggtaccaaga ttgtttcttt 2646

gtttcttttt ttcaaattgt gtttagaaat actgtaataa atatgcagta gtgatataaa 2706

gaattatatc caaggtaata taaaagccat tacgtatgaa ctcatccgtg tctcattttg 2766

tgttttattt tgtgatctct tgtccactaa gtatcttgtt aaatgccagt atctcagtct 2826

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aaaaagcttt tgt   2899

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<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala
1   5   10   15

Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu
                20   25   30

Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg
            35   40   45

Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly
        50   55   60

Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg
65   70   75   80

Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu
                85   90   95

Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr
                100   105   110

Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro
            115   120   125

Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val
        130   135   140

Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp
145   150   155   160

Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile
                165   170   175

His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys
            180   185   190

Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

                    195   200   205
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu
            210   215   220
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile
    225   230   235   240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe
                    245   250   255
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu
            260   265   270
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val
            275   280   285
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp
    290   295   300
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp
305   310   315   320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg
                    325   330   335
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp
            340   345   350
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly
            355   360   365
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln
        370   375   380
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val
385   390   395   400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly

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                    405                  410                  415
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp
              420                  425                  430
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys
          435                  440                  445
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu
          450                  455                  460
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His
465                  470                  475                  480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
                  485                  490                  495
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val
              500                  505                  510
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His
              515                  520                  525
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly
          530                  535                  540
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr
545                  550                  555                  560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg
                  565                  570                  575
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu
              580                  585                  590
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His
              595                  600                  605
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile
      610                  615                  620
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Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr

625   630   635   640

Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu

                    645   650   655

Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu

                    660   665   670

Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro

                    675   680   685

Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn

        690   695   700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (626)

<400> 107

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tctccttagt cgccgcc atg acg acc gcg tcc acc tcg cag gtg cgc cag   110

                    Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln

                    1   5   10

aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg   158

Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu

        15   20   25

gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac   206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp

    30   35   40

cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254

Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln

    45   50   55

tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302

Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn

60   65   70   75

caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350

Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys

      80   85   90

gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398

Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu

      95   100   105

gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446

Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr

     110   115   120

gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494

Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu

     125   130   135

aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542

Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn

140   145   150   155

ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590

Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe

    160   165   170

gac aag cac acc ctg gga gac agt gat aat gaa agc taagcctcgg   636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

                175   180

gctaatttcc ccatagccgt ggggtgactt ccctggtcac caaggcagtg catgcatgtt 696

ggggtttcct ttacctttc tataagttgt accaaaacat ccacttaagt tctttgattt 756

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<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp
  1   5   10   15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser
             20   25   30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala
             35   40   45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg
         50   55   60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg
65   70   75   80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser
                85   90   95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn
             100   105   110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro

               115   120   125

His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys

          130   135   140

Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly

  145   150   155   160

Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu

               165   170   175

Gly Asp Ser Asp Asn Glu Ser

          180

<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (256)..(1857)

<400> 109

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gggctgggct gtgcgcctgc gcagtgtggg tcgctcccga ttccctgccc cggccggccc 180

cgcctcggct ccgcaccctc gccccgctct cagccgccgc tctgccccgc agcagccagc 240

cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

                Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

                 1   5   10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339

Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

                 15   20   25

tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag   387
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu

            30   35   40

ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg   435
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met

        45   50   55   60

gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga   483
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg

                    65   70   75

cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc   531
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro

                80   85   90

acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg   579
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val

            95   100   105

gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag   627
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys

        110   115   120

ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag   675
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln

125   130   135   140

ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg   723
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly

                145   150   155

atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca   771
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala

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            160               165                170
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc    819
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu

        175               180                185
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc    867
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile

        190               195                200
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag    915
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys

205               210                215                220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc    963
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu

                225               230                235
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc    1011
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val

                240               245                250
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc    1059
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg

                255               260                265
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca    1107
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser

        270               275                280
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg    1155
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg

285               290                295                300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa    1203
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Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys
                   305   310   315

gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg   1251
Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val
               320   325   330

aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc   1299
Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile
         335   340   345

tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag   1347
Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln
        350   355   360

acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac   1395
Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp
365   370   375   380

acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg   1443
Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met
             385   390   395

gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc   1491
Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly
           400   405   410

gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag   1539
Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu
        415   420   425

ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac   1587
Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp
       430   435   440

aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc   1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
445   450   455   460

aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc   1683
Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
                465   470   475

ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag   1731
Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
                480   485   490

gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc   1779
Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
                495   500   505

aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac   1827
Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
                510   515   520

ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca   1877
Leu Val Pro Pro Ser Lys Arg Arg His Glu
525   530

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\<211\> 534

\<212\> PRT

\<213\> Homo sapiens

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Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

                20   25   30

Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro

           35   40   45

Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val

        50   55   60

Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu

    65   70   75   80

Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser

                85   90   95

Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn

           100   105   110

Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe

        115   120   125

Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro

        130   135   140

Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly

145   150   155   160

Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu

                165   170   175

Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His

           180   185   190

Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys

           195   200   205

Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile

        210   215   220

Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu

225   230   235   240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser
              245   250   255

Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu
              260   265   270

Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn
              275   280   285

Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala
         290   295   300

Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn
305   310   315   320

Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly
              325   330   335

Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp
              340   345   350

Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe
              355   360   365

Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp
         370   375   380

Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu
385   390   395   400

Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly
              405   410   415

Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu
              420   425   430

Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr
         435   440   445

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Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly
        450                 455                 460
Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val
465                 470                 475                 480
Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu
                485                 490                 495
Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu
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Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro
                515                 520                 525
Ser Lys Arg Arg His Glu
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gtgtgattaa cctccatttc agctaatc atg gga gag att aaa gtc tct cct     112
                              Met Gly Glu Ile Lys Val Ser Pro
                               1                   5
gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg   160
Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val
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                10                    15                    20
gat gat gat gac agt aag ata tgg tcg ctc tat gac gcg ggc ccc cga    208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg
      25                    30                    35                    40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca    256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala
                      45                    50                    55
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg    304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg
            60                    65                    70
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt    352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys
            75                    80                    85
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat    400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His
            90                    95                    100
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa    448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu
105                    110                    115                    120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc    496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser
                      125                    130                    135
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt    544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe
            140                    145                    150
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt    592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe
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406/527

                    155   160   165

tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg   640
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met

                    170   175   180

gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt   688
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu

        185   190   195   200

acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg   734
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser

                    205   210

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agaagaaatg tacaagctgt atccctaatg ccccgaagag gctcatctga aaacaggagg 854

caatttccca tacctgtgca gaagtgcaga ggtcaatctt tatgtacaga tacatttgtc 914

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<211> 212

<212> PRT

<213> Homo sapiens

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Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp
            20   25   30

Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
            35   40   45

Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
        50   55   60

Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
65   70   75   80

Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
                85   90   95

His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
                100   105   110

Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val
            115   120   125

His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
    130   135   140

Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
145   150   155   160

Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
                165   170   175

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly
                180   185   190
Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu
                195   200   205
Cys Gly Thr Ser
        210

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Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys
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kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa    96
Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys
                20                  25                  30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac   144
Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His
        35                  40                  45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc   192
Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala
    50                  55                  60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac   240
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Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

  65   70   75   80

ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca   288

Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr

                      85   90   95

atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt   336

Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val

                    100   105   110

ggc agc atg ggg gcc ctg ctc ttc tgagcccgtc tcccggacag gttgaggaag   390

Gly Ser Met Gly Ala Leu Leu Phe

                    115   120

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acactcacgc cctgtgggtg atggtcacgg tgggtgggtg ggggctgacc ccagcttcca 2310

ggggactgtc actgtggacg ccaaaatggc ataactgaga taaggtgaat aagtgacaaa 2370

taaagccagt tttttacaag g   2391

<210> 114

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (17)

<223> unknown

<220>

<221> unsure

<222> (18)

<223> unknown

<220>

<221> unsure

<222> (19)

<223> unknown

<220>

<221> unsure

<222> (31)

<223> unknown

<220>

<221> unsure

<222> (109)

<223> unknown

<400> 114

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

  1   5   10   15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

               20   25   30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

          35   40   45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

     50   55   60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

```
        65                  70                  75                  80
```

Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr

```
                      85                  90                  95
```

Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val

```
                 100                 105                 110
```

Gly Ser Met Gly Ala Leu Leu Phe

```
                 115                 120
```

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

gggtatggaa ttggctgagg atcaaacgta tgtaggtgaa aggataccag gatgttgcta 60

aaggtgaggg acagtttggg tttgggactt accggggtga tgttagatct ggaacccca 120

agtgaggctg gagggagtta aggtcagtat ggaagatagg gttgggacag ggtgctttgg 180

aatgaaagag tgaccttaga gggctccttg gcctcagga atgctcctgc tgctgtgaag 240

atgagaaggt gctcttactc agttaatgat gagtgactat atttaccaaa gcccctacct 300

gctgctgggt cccttgtagc acaggagact tgggctaagg gcccctccca gggaagggac 360

accatcaggc ctctggctga ggcagtagca tagaggatcc atttctacct gcatttccca 420

gaggactagc aggaggcagc cttgagaaac cggcagttcc caaagccagc gcctggctgt 480

tctctcattg tcactgccct ctccccaacc tctcctctaa cccactagag attgcctgtg 540

tcctgcctct tgcctcttgt agaatgcagc tctggccctc aataaatgct tcctgcatt 599

<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

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<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t


<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

ttcgatcaca tagttcctca ttcccaccga agtgcatgaa atggcagtag aaatcactat       60


acagtgcttc caggggtgca ttggtgggaa tgagaatagt gatgaagtag aaatgtctgc      120


cacagttcca gganngggta ggtagcagtg tgtgtgttat gtgccactga ccctgaaara      180


tgtgccatag cccaagccaa ttgaaattga tcaggggggcc aggcatggtg gctcatgcct      240


gtaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga      300


ccagcctgtg caacatagca aaaccccatc tctacaaaga ttaaaaataa aaaattagct      360

gggc                                                    364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(217)

<220>

<221> unsure

<222> (37)

<223> a, c, g or t

<400> 117

gttcagtttc aagtttacaa gaggc atg gat gga gtn gtg acg ttc ttg aca      52
                                Met Asp Gly Xaa Val Thr Phe Leu Thr
                                 1               5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg     100
Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser
 10              15                  20                  25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg    148
Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly
            30                  35                  40

cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt    196
His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe
            45                  50                  55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg       247

Pro Ala Phe Gln Leu Asn Ala

      60

atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307

gtttaactca gtctgtttaa aaacaaactt ttctggtggt tgataacaga gagttgctcc 367

ctgagccatc agggtcctgg gagctggaag tgaaagggtt attaacattc tacctttatg 427

cagctgttgg ctgaccagaa taaactccct gctgagttca agctttgaat ggaatggatg 487

caaatgatgt tgtttccatt agagcaggtg ctcacagcat tctgattggc ctgagcagac 547

cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaacctcact 607

cacccctctg gcctctacag ccctcagagg agagaaaacc aattctccaa caaacaggtc 667

tctccaacat ggtggtgctg gcaggcttag gtttagaaaa tcctgactgt taaaggcgtt 727

tgaatacatc acattcctat gcaaatgttt ttaatctcca gtttaatgta gtttattttt 787

cctatatgta aagtattttt atacggcttg tatcatgata gtttagcaat aaaacagttg 847

gaagc                                                    852


<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1               5                    10                   15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

      20                   25                   30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

            35                    40                    45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

            50                    55                    60


<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222>   (524)..(1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

cggcaactgw gaggaagcaa agggaaaaaa actccattaa aaagcccagc tttcctccat 60

gttagatgtg acttggaaaa tgagaaagat ttagcaaaat tccaccgtat cttttgccag 120

gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180

aagcccctcg aattctgtga aaatgagggt ttcttaactc acactgagag cggaaagggg 240

cagacccttt tcataactcc ctcaagtgtg tgttaccttt ctttaccagc atggtaagca 300

acaggacata tcccagcctc ggacatgtct gtatgatcca aggtacccaa agtcagacag 360

agtaaactca agcctggcac tggctttctg ccgcttcatg tgctttggaa aaagcaggag 420

aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480

actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt    535

                                                  Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc    583
Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5                 10                 15               20

tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac    631
Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
             25                 30                 35

cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga    679
His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
         40                 45                 50

ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc    727
Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
           55                 60                 65

tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac    775
Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
    70                 75                 80

cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag    823
Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
85               90                 95             100

gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat    871
Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
                105                 110                 115

ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag    919
Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu
         120                 125                 130

aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga    967
Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly

       135               140             145

gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa   1015

Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys

       150               155             160

gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag   1063

Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys

165             170             175             180

aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc       1105

Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile

             185             190

tgaggttgtc tgggacctgc ctccacccca tccagggatg agaatggcag c   1156

<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys

  1            5               10              15

Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro

          20              25              30

Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln

         35               40             45

His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln

     50               55             60

Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe

65             70             75             80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val

                    85                  90                  95

Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly

                   100                 105                 110

Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu

              115                 120                 125

Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala

           130                 135                 140

Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln

145                 150                 155                 160

Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His

                   165                 170                 175

Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser

                   180                 185                 190

Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

g gac att gag tcc aag gag cag gtg cgn acc ctc acg ggc cac gtg ggc    49

  Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

    1                  5                   10                  15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc    97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

                    20                    25                    30

ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac   145
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

                    35                    40                    45

atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg   193
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

               50                    55                    60

ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act   241
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

     65                    70                    75                    80

gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc   289
Val Lys Val Trp Thr Cys

                    85

cctgaaccag ccctggacct ttctgagcca ggctggccac atggggtggt ctcggggttt 349
ctgcctgccc cgtgggcata ggtggacagg ctctggcarg ccggcagtgc cctccccgtc 409
ccatgctcgg cgagcctccc tctactcggc actgtccttg ctgcccagcc cctctctggg 469
tgccaggtac gacgcttgcc ccggcccacc ctccatcccc accctccatc cccaccctag 529
atggagcgag ggcctttta ctcacctttt ctaccgtttt tagactgtat gtagatttgg 589
ttacctcctg gttgaaataa atgctccaca gactgtgaaa awaaaaarrr acaamtcctc 649
gggacaaggg ggctgtgtgt ggccttgagg ttggtgtgca caggcactgg ctgctgtgag 709
tggggggca tggggcagtt tcctttggtg gaccccagga cttcggccca ctccggggct 769
cccctccctg ctaggaggca actcgtcaca cccaagctgc tggcctccag tcccatctcc 829
cccaacacat gtgcccccaa aaagtgagcc aggcacctct gtttcctgct gtttattgac 889
agccgacgga gcgccttgcc cagacctccc ctgcccacct gctggagccc agcctgtgcc 949
gccctctgag gagaggcctg gggggacagc tgggcacgtc cactcgcagg gaaacacggg 1009
gtgagacagc aggaaggggc cctgcacgcc gggacgccac ctccgccagc cgcctccacc 1069
cgccccacac cacaatcgct ggttttcggc attttttaaa ttttttttt aagaaacgtc 1129

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aaagttgtgc ccaacactgt ggatcagcaa acacgataga ggagaccagt cagtacttct 1189

tggagggggc aggaggagag aggaaaaggg agggcgagaa tgaccacaca acacagcctt 1249

ggaccatgag cagaagcgtc cgtgggaact ccactggggt ggatgggctg cctgcacagc 1309

ccctggagag ggggccaggc acaccctcag agggagctgc aagcccgtgg cctggcctgc 1369

tacatgccct gcttccacgt ggctgccacg ctgacacacc cacattcacc aaacccaccc 1429

gcgccctggg acgcagccac gccaggagga ggacacggcc gccgagagca aggcacaacc 1489

tcgagttctt ggggcgcaga gaacttagga gagaagcacg gaggagcccc cggcagagca 1549

cccgcccccg ggccccagcc ttccacctgt gctagcagcc tggggcctcc actctggccg 1609

gaggaaggac cgcaggcaga cagcctgggc ctctaacagc ttttgtccgg agctagactt 1669

cgtgtccttt cagttggtaa atggttttct atagaatcaa taatatttct ttctttaaat 1729

ata   1732
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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

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Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly
1               5                   10                  15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val
                20                  25                  30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn
        35                  40                  45
```

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

     50   55   60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

     65   70   75   80

Val Lys Val Trp Thr Cys

          85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168)..(350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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acagatgtga cccaggctta ctaaagagac aactccacag ccctgggaac acactcttga 120

gccaaacttg gttgaagact aggtcttccc tggcaagttc cggaaga atg gac tta   176

                                                      Met Asp Leu

                                                        1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg   224
Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

        5   10   15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt   272
Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20   25   30   35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt   320
Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

                40   45   50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcct   370
Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

                55   60

tccacacggt gggaaggatc ttgctgcttt cactcacagg accagggagt tyttcaatca 430

ggaggtgggt ttttgttccc ttcaggsctt tggcaacatc tagagacagt tttgattgcc 490

acgcctggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tcctacactg 550

cataggatag tccccactac ccccagccaa gaattatctg actccagggg tca   603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln
 1   5   10   15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly
                20   25   30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr
            35   40   45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser
        50   55   60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775)..(1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

tatgcgagcc aatattgaga gaggaatttt gctgaggttt tctctgaggt tttttttgatg 60

ctttatagga aactattttt taaaaaaagc catttcccac ccaaggacac agtggatgtg 120

ttttccctga ctccagcagg gcaaggaatg taaccgagag gttgtgtggg ctgggctctg 180

gtgccctctt ccctggcccr gaacacctct cctcctgatt cccttggcac cttgtctttc 240

tgtctgttta cctgtctccc tgcctgccca tctgcatctt ttgcagccca ctctgacttc 300

catctggggg ctgagaccac ccttgcctgc ccccttcttt ctgccttaag aatgtccttt 360

taggctgggc atggttgtca cgcctgtaac cccagcactt tgggaggcgg agacgggcag 420

ataacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaact ccgcctctag 480

taaaaataca aaattagccg ggcatggtgg tgcacgcctc taatcccagc tactcgggag 540

gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600

ccactgcact ccagcctggg caacagagcg agactccgtc ttaaaaaaaa aaaaaaaaag 660

aacgcccttt tactgtcctc atcatcccag tttgaggcag tgctggagtg gggaaggccg 720

tcttagacca tagaggttgg aagacgctga gagatcatcc agcccagccc cttg atg   777
                                                                Met
                                                                1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac   825
Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His
            5   10   15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag   873
Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln
            20   25   30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca   921
Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr
        35   40   45

tca tgt ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg   969
Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp
50   55   60   65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga   1017
Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

```
Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly
                    70              75              80
```

```
tgacagacag cttgcccgca cactcgggcc ccactcaagg atgtagggcc ttttctggcc 1077
cctgacccct ccctgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137
ggggcatcac ctccttctgc tgcttctccc tgctcctacc ctcaagggcc tgggggctgc 1197
ccagctgcct ctatgccctt ctgggggtct cagcccactg ctgacacttc tgcaatccag 1257
agaaacacta aataaagcaa tacgtgtttg cc                              1289
```

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

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Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala
 1               5               10              15
His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro
                20              25              30
Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro
            35              40              45
Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro
        50              55              60
Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu
65              70              75              80
Gly
```

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734)..(886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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caccacaacc tctgcctcct gggttcaagc gattctcctg ccttagcctc ccgaatagct 120

ggaattacag gcacgcacca ccatgcctga ctaattttgt attttagta gacatggggt 180

ttctccatgt tggtcaggct ggtctcaaac tcccaccttc aggtgatccg cccacctcgg 240

cctcctgagg tggctgagat tacaggcgtg caactkgtgc cagcttgcta attttcacag 300

aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatttt 360

ttgaagccag tactgtgctc tgcatataac aaagctgctt caaggatgag acctttttct 420

aaaagcatgt aatgtgagaa gccggcctgc cttattttct tttttctttt ttaatgatta 480

aaaatagttt gtggcaaggc acggtggctc aggcctgtaa ttctagcact ttgggaggcc 540

gaggcaggag gattacttga gcctacaagt ttgatgggcc agcatgcaca gcatagcaag 600

actgcatctc tacagagagt aaaaaaaatt acccgagtgt ggtgatgtgc atctgtaatc 660

tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720

gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga   769

                    Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

                      1   5   10

ccc tgt ctc aaa aaa aaa aaa aat ata tat ata tat ata tat tat ttt   817

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Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe
            15                  20                  25

tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga    865
Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly
        30                  35                  40

acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt       916
Thr Ser Trp Lys Thr Thr Pro
    45              50

gattcctgct ttcagaagga ggtggattca aatacatcaa aagtcccttc ctctgctaag 976
tgtttatagt tcaatgaata atttcaatat ttgtatgtgt tcttgtcatt ttattttttt 1036
ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt              1085
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<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

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Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys
    1               5                   10                  15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys
                20                  25                  30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys
            35                  40                  45

Thr Thr Pro
        50
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<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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gctttgaact tactcaggaa agccagcccc cataatattg tattaccaaa cagtatcgct     60

ttgttaggaa ggatctggaa taatcttgaa gggaagtcag agttttctcc ctgcctatta    120

acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag gtagggccaa    180

attaactctt gtggacagtc cctaaaagtc cagttctaca tttgtgaaaa ttgtggtgcc    240

atgaattaag atggatgact ggaaaaaggt gttggagaaa gagttaaaga tgaggaagag    300

atattttag tatatgaagt tatccaggga cttgatattc ataattcagt gctgtggaaa    360

tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa    420

agaagtctga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttccaaa    480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg    540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg    600
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ttttttgctag tcccacccccc attttagcct aatttggctt aaacgcagta tggggagaat      660

tgttcccatt ccatgtgttc tgaattcagc tcatctccca gcatatagat atatcctcct      720

ttaactccga ccagaaccct tcttcctgtg gcactcccca cccatagacc ttcagatcat      780

ctcccacacc ctggatctca ctctcctctt agtaacagag acactcctga ggttggactt      840

ccttgctttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccgagt      900

aagcagggat gtactagggg aatgtaaaac tgcaaactta aaaacctgca tcttcttgaa      960

gcatcagttt tacttaccaa atggtttaga gtcataagat gacctatttt tatataaaag     1020

ttatattata gaataaaatg ttcatacgca tagactgtta agataaaaaa ataggraatc     1080

ttgcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatggt     1140

attttggtgt tcacttacga agcatacaac tagaaccata tccaagcaga ctctgggttg     1200

ctgttaaccc agggcctaga cttctagtgc ctctgaggca gaaccaaagg agcctgcact     1260

gggggaaatc cctttttcctg cctgcctgtc tgcctgtgac ctgtgtacgt attacaggct     1320

ttaggaccag ctgattgtta tgcttgcagg atggttttga aacagaaaca atacttgttt     1380
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actgtaggaa tcctatttat attatttttc agtcctgtga atgctgtgaa aagatttatt   1440

cctttgaggc caggaagctc ccaggcatat atgcttctag gttaggattg tcctgactca   1500

ctaaagatgc caggatattg gggctgaggg gagtttgagg tgtt   1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

tgaaatcagg gctggagctt tacttaggat tcacatggcc tcctaggaac catgggacaa   60

atgggaaaca ggttatcggg ggattcatga agtcagtgag agtaattgct tcttttttgc   120

gggtgaactg aatgtatttc ttcaccaaat cttgatgtta acaattaaaa agaagaaatg   180

acatgcaagt aggtcttagc agaaaaatgc aggctgggca tgagtcatgt tgttaccctc   240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt   300

atttggtatc tcaaattttt cgtcactgtt cacatgccac tttctctgtg cacagtggta   360

tcctcatttg ctttttaacc tacactgagg agtctttgtc aggttgcact gattttccaa   420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtcc aatgaagttc   480

tctaaattat tttaacattg cctttgaa   508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

⟨223⟩ a, c, g or t

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (417)

⟨223⟩ g or c

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (419)

⟨223⟩ t or c

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (430)

⟨223⟩ a or t

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (448)

⟨223⟩ t or c

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (449)

⟨223⟩ g or t

⟨220⟩

⟨221⟩ unsure

⟨222⟩ (472)

⟨223⟩ a, c, g or t

⟨400⟩ 131

ggcccctggc aatttgcctc aagatggggg tttgaaaata actttacctk actsaaggag   60

tgtctggagc acctcctagt ctaagtctgc aagctccagt tcttgcctaa aaccatgcca   120

gtggccaccc ttgggctcag acagctctgg gccttttgac cacaagccag cccctcgccc   180

tctctgtggc atagtcttct ctgccccagg actgcagggc ggcttcctcc aaggcttcca   240

aggctcaaaa gaaatttggc tccatccaag aaggctccag ctcccctact ggcccctggs   300

ttcaggccca cacccctggg ccagggccag agagtgtgtc tcaggagaat tcaatgggct   360

ctagagagac acacagaaag tttgggcatt tgggaaattt tcaaggrtgt atgtntsgyt   420

cacgtatggw gcaggttgtc ctggtccykg ggtgcaggga agtgggctgc anggaagtgg   480

attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg   540

acagccccaa ggttgggaag acctggcctt agtcgtcctc agcctagggg cagggcagtg   600

aagaaagctc tccccgctcc tgctgtaatg acccagagta gcctccccag gccggcatct   660

tatgtgtgtc ttccaccatc ctcatggtgg cacttttcta ggcctgtctc ccagcattgt   720

gcaaggctcg gaagagaacc agggaagtga aactgggtga aaacagaaag ctcaatggat   780

gggctaggtt ccccagatca ttagggcaga gtttgcacgt cctctggtca ctggaatcca   840

cccagcccac gaatcatctc cctcttgaag gattttattt ctactgggtt ttggaacaaa   900

ctcctgctga daccccacag ccagaaactg aaagcagcag ctccccaaag cctggaaaat   960

ccctaagaga aggcctgggg caggaagtgg agtgacaggg gacaggtaga gagaaggggg   1020

cccaatggcc agggagtgaa ggaggtggcg ttgctgagag cagtctgcac atgcttctgt   1080

ctgagtgcag gaaggtgttc cagggtcgaa attacacttc tcgtacctgg agacgctgtt   1140

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cctg   1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

cccgggagaa tcacttcagc ctgggagatc aaggctgcag tgagctctga acgcaccact   60

acactccagc ctgggtgaca gagtgagatc ctgtctcaaa aaaagagaaa gaaaaccttt   120

gagattcttc cattttttaga gctgagagag cacttgtgaa acacacacac atgcacaaac   180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc   240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat   300

tcctaggaat atgccaaagc ttttcaaagc ctctatggac agctcattcc ttaactttc   360

ctctttaaaa tctttttttan cttcttattt gccccagcca ctatcactgc ctcaggcagc   420

tgcaacgtta aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt   480

gtgtattgaa tgggtatcaa gtcacgtc   508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

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tcttggagag ggatggagac tgaagagtga gtttggtcct ccacttgatc caggttctta   120

ttttttgtttt ctacttcaaa gcgagaactt ggtactgtga ctttgataag aattgacttc   180

aggcccagca agatccctca tgcctgtaat cccagcactt tggggggcca aggcaggagg   240

attgcgtgag cccaggagtt cgagacccac ctgggcaaca tagggacctt gtctctacaa   300

aaaataaaat tanctgggtt tgatggtgca catcastggt cctggctact cgggaggcca   360

aggtgggagg aatgcttgag gatcggaggt caaggctgca stgagccaat attgtgccac   420

tgcattccag cctgggcaac agagtgagac actgtcttaa aaaaaaaaa aaaaaacggt   480

ccgc   484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

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tacacagcat ttttaacacc ttttttttct agttttttttg ttcggttttg ttttccatca   120

ggaatttgag ttctctctaa cccagcttac tgtgggacat aggaaaactc agtagaaata   180

cctttggtga tcttgttgag tttaagtctg atcttgatct taaactcagt aagccactat   240

ctgcaatttt gtacattata tagtattttg aagatatgga accttatgaa aaaaaaatag   300

caaattagtt cttttccccc cagaggggaa agttatgttc tgcaaatagt gtgtgtctta   360

ttttactgtt gaacagcaat tgctatttat ttttttattg cctagaactt caacatgttg   420

tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gttaccatca   480

aacatcagta cacttgtcat ttcacatgtg tttaatgtga cagtttttca gtactgtatg   540

tgttaatttc tacttttttt aatatttaaa attgctttta aataaacata ttctcagttg   600

atccc   605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

g gca cga ggg tcc tct gca tgg ggt cag gtg ctt ctg tgc ttg ctg tcc   49
  Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser
  1   5   10   15

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tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg    97
Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu
                  20              25              30
gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc   145
Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile
              35              40              45
agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac   201
Ser Cys
      50
cttcttgagt agccactgtc tgccagccac tgctctagag atgggaaaac agcacggaac  261
aaaaccaagg tctttcttcc agcgaattta tatccttcag gaagctggtt cctgccacca  321
acttagcagg caacagttct cctcccctag tgggcacagg gtaccagttt tgtaggaaaa  381
gtggtccagc aaaggaagaa agcagaccaa cccagctgcc ttaccttatt ctggggccat  441
tcccccagcg atgagagctg ctcttgtttc tactgccacc atctcttctg gctgcacttc  501
acctgctgct tgagcttctg accttccttc agttccacca aatgaggaca ggaaatagca  561
gtcaagaccc ctgggccctg ctgagcgtga aacaggaagg caatgggatg agttgctggg  621
acggaagaat gggcctgggg cagaacaaat agggagcatt tgaaagcttc tggctgataa  681
atctccaggg tgcatcccgg ttgccacgcc tgcccccatt aacctgctcc tggtaaatac  741
tgatccagca gctgctccag gagaggccgt cttttttttc ccagccacgc tgtgtctttg  801
catgagactc cttggggcct gggcacagag agaaaagaat tgagactcag gaggctcagt  861
gggtgagaaa atgcaaagtg gcttcacaga cacagggctg tgggagcaga tcgacgggga  921
acttgggaga tgaacttcag ggccttccga cgccttgtct caggaacatg ctttgagaaa  981
aatggtagca tcctttccat aactcagtct ctcttcccta gtttccctga agtgtgacgt 1041
tttagtatct ggagctcagt gatccccatg aatgagggat aaagtttcac tcttggtatt 1101
ttctaactag tgctagggaa agtcctgaga cacgatcaca gccactgctt ggcatacagg 1161
gcctccaccc aataagcaaa ctggagattc ctcagcctct cgtggacacc cacatctcat 1221
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tcttctcaca gcagagaagc tctcccttca gcctgagctg tcttctttct gctgcagtgc 1281

agcctgctcc ctcctaccct ggcctcaagg aaggtgggaa acatcttctg catttcaaag 1341

tcctcacttt gacttatttg gccttcatct tggcatggaa ggtggcaggc agaatggaaa 1401

tacctccccc caaacaaaac agatattctt gcgtgtgtaa gggcagaagg gacaagctct 1461

ctatcccatg agactagggg ccggagccca cctgcctttc cccacaactt ttcctgctca 1521

aacccactcc tcttgacaca ctggaatctg tattatatat attttttaaga aaatacaatg 1581

atggttgtct ggttttgttg tttttacagg tgttgtggaa taaaaactgt aagaaaatta 1641

agtatttaaa atgttccaat aaagtggggt tttttgttat tctaatatat tattgtgtac 1701

ctattgtaaa tatgaaacac tcctattttg caagctgagg acacaatttg tactgttgtt 1761

atatataaat aaagtttact gaatt   1786

<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

  1   5   10   15

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

            20   25   30

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

            35   40   45

Ser Cys

    50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535)..(729)

<400> 137

gaaaaatctc attatttcaa aatgatagac atataccaaa aacaagtcta taatgtgagt 60

agttactaaa atttacacat cttaaaagtg tgtaaatgct taaatttcag aattaccatc 120

agaacctcaa ttgacattcc tttgaatagg ctaataagtg acaaataaga ttaataagat 180

ttttcaaaat cgccaggact ggtgaatata aatgatgatt gaactggaat aatattgggg 240

accaaatcaa atgaatgatt aaattatgaa gctcatatcc ttttgaaggt agttgcaaag 300

agacatttca aaactgccct aggccattgc agcatcctta gatgggacgc ataatcatta 360

ccttaaagca tcaccactca ttttgaccat atagatttta ttatgttagt ttaaaaggtc 420

aatcagcctc atgactttat agttatgtct tgtatttaaa aacatttttt atacatttgg 480

ttatgttgat aaaccaaaaa catttgatta ataaaatatc tatttgaata aatt atg 537
                                                                Met
                                                                  1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585
Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr
                5   10   15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633
Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr
            20   25   30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681
Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu
    35   40   45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

        50   55   60   65

taaatccagg ctttatgtac aaacatgttg tttgttttat ttggggctgg gggaggtata 789

tgatgagcag acttctcgga attcataata aattttctaa aagcct   835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

     1   5   10   15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

                20   25   30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

             35   40   45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

        50   55   60

Lys

 65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac   48
Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

    1   5   10   15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg   96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met
                20   25   30

gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat   144
Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
                35   40   45

aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct   192
Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
        50   55   60

atg aaa cac tgaagagaaa tgtaggcaga aggaaatggc cacatatcac   241
Met Lys His
    65

aagttctatt atatattctt ttgtaaatac atattgtata ttacttggat gttttcttat 301
atcatttact gtctttttga gttaatgtca gtttttactc tctcaaytta cwatgtwaca 361
twgtaartaa cataatgtcc tttattattt atatttaagc atctaacata tagagttgtt 421
ttcatataag tttaagataa atgtcaaaaa tatatgttct tttgtttttc tttgctttaa 481
aattatgtat cttttccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541
gtatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601
taaagaattt attattcaaa atact   626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn
    1   5   10   15

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

                20   25   30

Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

                35   40   45

Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

            50   55   60

Met Lys His

    65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(525)

<400> 141

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tcactctgtt aaagctggtc tgttctaact gagatgacag tc atg tcc ctt tcc   114

                                                Met Ser Leu Ser

                                                    1

agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta 162

Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu

    5   10   15   20

aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210

Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val

            25   30   35

gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser

        40   45   50

ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc   306

Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser

          55   60   65

cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata   354

His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile

        70   75   80

ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca   402

Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr

85   90   95   100

gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg   450

Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu

          105   110   115

gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta   498

Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val

          120   125   130

ttc tgt att act gaa aag gga gtg gtt   525

Phe Cys Ile Thr Glu Lys Gly Val Val

          135   140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

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      1                5                    10                     15
    Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val
                      20                    25                     30
    Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu
                35                    40                    45
    Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile
                50                    55                    60
    Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val
    65                70                    75                     80
    Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys
                            85                    90                    95
    Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly
                      100                   105                   110
    Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro
                115                   120                   125
    Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val
                130                   135                   140
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<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138).. (1307)

<400> 143

gagacttggg ctggagccgc cctgggtgtc agcggctcgg ctcccgcgca cgctccggcc 60

gtcgcgcagc ctcggcacct gcaggtccgt gcgtcccgcg gctggcgccc ctgactccgt 120

cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac   170
              Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
                  1   5   10

ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg   218
Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
              15   20   25

cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg   266
Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
          30   35   40

gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag   314
Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
      45   50   55

gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc   362
Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
60   65   70   75

aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc   410
Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
                  80   85   90

aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg   458
Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
              95   100   105

aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc   506
Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
          110   115   120

tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc   554
Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

```
           125                  130                  135
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct    602
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro
   140                  145                  150                  155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc    650
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr
                      160                  165                  170
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg    698
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp
                  175                  180                  185
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat    746
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp
              190                  195                  200
gtc atc cgt ggg tct tta agc ctc acc aac ctt tcg tct tcc atg gct    794
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala
          205                  210                  215
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt    842
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys
220                  225                  230                  235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct    890
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala
                  240                  245                  250
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg    938
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu
              255                  260                  265
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat    986
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Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn

        270   275   280

gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag   1034

Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys

        285   290   295

agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc   1082

Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser

300   305   310   315

gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg   1130

Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu

                320   325   330

acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg   1178

Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu

                335   340   345

ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt   1226

Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly

                350   355   360

ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg   1274

Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met

        365   370   375

gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327

Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

380   385   390

ggctaaagga tttggggtct ctccttccta taagggtcac ctctagcaca gaggcctgag 1387

tcatgggaaa gagtcacact cctgaccctt agtactctgc ccccacctct ctttactgtg 1447

ggaaaaccat ctcagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1507

ctggaattgg gaggagcctc cacccacccc tgactcctcc ttatgaagcc agctgctgaa 1567

attagctact caccaagagt gaggggcaga gacttccagt cactgagtct cccaggcccc 1627

cttgatctgt accccacccc tatctaacac cacccttggc tcccactcca gctccctgta 1687

ttgatataac ctgtcaggct ggcttggtta ggttttactg gggcagagga tagggaatct 1747

cttattaaaa ctaacatgaa atatgtgttg ttttcatttg caaatttaaa taaagataca 1807

taatgtttgt atgagataag 1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
1   5   10   15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
                20   25   30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
                35   40   45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
        50   55   60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
65   70   75   80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
                    85   90   95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
                100   105   110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
                115   120   125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
 130   135   140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
145   150   155   160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
    165   170   175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
    180   185   190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
    195   200   205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
  210   215   220

Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
225   230   235   240

Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
    245   250   255

Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
    260   265   270

Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
  275   280   285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
  290   295   300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp
305   310   315   320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
    325   330   335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

        340   345   350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

        355   360   365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

        370   375   380

Gln Ala Gly Ser Leu Val

385   390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)..(2726)

<400> 145

tgcgggaagc gatgtagtag ctgccaggct gtcccccgcc ctgcccggcc cgagccccgc 60

gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

                          Met Lys Lys Gln Phe Asn Arg Met Lys Gln

                          1   5   10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt   161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

        15   20   25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata   209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

        30   35   40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat   257
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His
        45   50   55

ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt   305
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu
        60   65   70

gct caa aat atg caa gaa gca tcg act cag ctg gaa gac tct ctc ctg   353
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu
   75   80   85   90

ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc   401
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu
                95   100   105

gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct   449
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro
                110   115   120

ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg   497
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg
                125   130   135

aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg   545
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg
        140   145   150

tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca   593
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro
155   160   165   170

tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa   641
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys
                175   180   185

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg   689
Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met
          190   195   200

gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc   737
Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala
          205   210   215

caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc   785
Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu
          220   225   230

ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt   833
Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe
235   240   245   250

ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg   881
Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala
                    255   260   265

ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag   929
Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys
          270   275   280

gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag   977
Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys
          285   290   295

ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat   1025
Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr
          300   305   310

tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa   1073
Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu

315   320   325   330

ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa   1121
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln

                335   340   345

gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga   1169
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg

        350   355   360

aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg   1217
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu

            365   370   375

atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg   1265
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met

    380   385   390

act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc   1313
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala

395   400   405   410

aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat   1361
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His

                415   420   425

gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc   1409
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe

            430   435   440

cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc   1457
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr

        445   450   455

acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg   1505
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser

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        460                     465                    470

ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga    1553
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly

475                     480                    485                    490

gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag    1601
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln

                        495                    500                    505

gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct    1649
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala

                510                     515                    520

ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct    1697
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala

                525                     530                    535

ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg    1745
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly

                540                     545                    550

ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc    1793
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser

555                     560                    565                    570

cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct    1841
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala

                575                     580                    585

gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat    1889
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn

                590                     595                    600

cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct    1937
```

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro

     605   610   615

cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa   1985

His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys

     620   625   630

aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac   2033

Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His

635   640   645   650

ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg   2081

Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu

         655   660   665

tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg   2129

Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr

         670   675   680

ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc   2177

Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro

     685   690   695

cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca   2225

Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro

     700   705   710

ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc   2273

Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro

715   720   725   730

aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga   2321

Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly

         735   740   745

ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt   2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser
            750   755   760

act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc   2417
Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr
            765   770   775

ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta   2465
Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu
         780   785   790

ccg aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc   2513
Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro
795   800   805   810

cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc   2561
Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu
            815   820   825

acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc   2609
Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser
            830   835   840

agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac   2657
Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp
            845   850   855

tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat   2705
Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn
            860   865   870

gat acc gag agc act gcc ctg tgaagaaagc cctttcccag ccctccacca   2756
Asp Thr Glu Ser Thr Ala Leu
875   880

cttccaccct ggcgagtgga gcaggggcag gcgaacctct ttctttgcag accgaacagt 2816

gaaaagcttt cagtggagga caaaggaggg cctcactgtg cgggacctgg ccttctgcac 2876

ggcccaagga gaacctggag gccaccacta aagctgaatg acctgtgtct tgaagaagtt 2936

ggctttcttt acatgggaag gaaatcatgc caaaaaaatc caaaacaaag aagtacctgg 2996

agtggagaga gtattcctgc tgaaacgcgc ataggaagct tttgtccctg ctgttaatgc 3056

gggcagcacc tacagcaact tggaatgagt aagaagcagt gcgttaacta tctatttaat 3116

aaaatgcgct cattatgcaa gtcgcctact ctctgctacc tggacgttca ttcttatgta 3176

ttaggaggga ggctgcgctc cttcagactt gctgcagaat cattttgtat catgtatggt 3236

ctgtgtctcc ccagtcccct cagaaccatg cccatggatg gtgactgctg gctctgtcac 3296

ctcatcaaac tggatgtgac ccatgccgcc tcgttggatt gtcggaatgt agacagaaat 3356

gtactgttct tttttttttt tttaaacaat gtaattgcta cttgataagg accgaacatt 3416

attctagttt catgtttaat ttgaattaaa tatattctgt ggtttatatg   3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val
1   5   10   15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile
            20   25   30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys
        35   40   45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg
    50   55   60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

                65   70   75   80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr

                        85   90   95
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu

                        100   105   110
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu

                        115   120   125
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu

                130   135   140
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys

145   150   155   160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu

                        165   170   175
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp

                        180   185   190
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr

                        195   200   205
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg

                210   215   220
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His

225   230   235   240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu

                        245   250   255
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys

                        260   265   270
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg

                275   280   285

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp
        290   295   300

Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val
305   310   315   320

Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met
                325   330   335

Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp
                340   345   350

Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro
            355   360   365

Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys
        370   375   380

Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala
385   390   395   400

Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu
                405   410   415

Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu
                420   425   430

Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe
            435   440   445

Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His
        450   455   460

Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys
465   470   475   480

Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu
                485   490   495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly
         500   505   510

Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro
         515   520   525

Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro
         530   535   540

Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser
545   550   555   560

Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro
            565   570   575

Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg
         580   585   590

Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala
         595   600   605

Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro
         610   615   620

Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro
625   630   635   640

Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser
            645   650   655

Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr
         660   665   670

Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln
         675   680   685

Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser
         690   695   700

Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr

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     705                    710                    715                    720
Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro
                    725                    730                    735
Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His
                    740                    745                    750
Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys
                    755                    760                    765
Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro
     770                    775                    780
Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val
785                    790                    795                    800
Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro
                    805                    810                    815
Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr
                    820                    825                    830
Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His
                    835                    840                    845
Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val
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Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala
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<211> 3021

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<400> 147

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ctctgctaag accgctgcc atg cca gtg acg gta acc cgc acc acc atc aca   172
                      Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr
                       1   5   10

acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg   220
Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly
              15   20   25

tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag   268
Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln
           30   35   40

ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc   316
Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala
        45   50   55

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc   364
Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 60   65   70   75

ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag   412
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln
                 80   85   90

gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc   460
Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

                    95   100   105

tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc   508
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr

                    110   115   120

tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc   556
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala

                    125   130   135

gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg   604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val

         140   145   150   155

gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc   652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr

                    160   165   170

gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc   700
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile

                    175   180   185

ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg   748
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu

                    190   195   200

gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc   796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile

                    205   210   215

gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc   844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro

220   225   230   235

ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat   892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr

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             240                    245                    250
gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat    940
Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr
              255                    260                    265
ggc ggc cag cct cgg cgc tcg aga gat gta agc tgc agc cgc agc cat    988
Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His
              270                    275                    280
gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg   1036
Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu
            285                    290                    295
acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc   1084
Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
300                    305                    310                    315
cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttccct   1135
His Leu Val Phe Val Lys Val
                 320
ctccaacctc tttgttcttc ttgcccgagt tttctttatg gagtacttct ttcctccgcc 1195
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<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

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Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
           35   40   45

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
       50   55   60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
65   70   75   80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
             85   90   95

Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe
             100   105   110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
            115   120   125

Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser
          130   135   140

Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala
145   150   155   160

Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu
             165   170   175

Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser
           180   185   190

Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala
          195   200   205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn
        210   215   220

Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
225   230   235   240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val
                     245   250   255

Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg
                     260   265   270

Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys
             275   280   285

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu
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Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val
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Lys Val

<210> 149

<211> 4409

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<222> (39)..(2027)

<400> 149

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                                        1   5

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Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln
          10   15   20

gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt   152
Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser
          25   30   35

cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa   200
Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys
          40   45   50

gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg   248
Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu
   55   60   65   70

gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag   296
Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys
                  75   80   85

aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa   344
Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys
              90   95   100

gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt   392
Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly
          105   110   115

tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att   440
Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile
          120   125   130

gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag   488
Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys

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        135                 140                 145                 150
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac   536
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr
                155                 160                 165
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa   584
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys
                170                 175                 180
gaa aca gct cca ggt ggc act gaa tcg cag tca ctt aga aca aat gaa   632
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu
            185                 190                 195
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa   680
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu
        200                 205                 210
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc   728
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile
215                 220                 225                 230
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc   776
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser
                235                 240                 245
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct   824
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro
                250                 255                 260
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac   872
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp
            265                 270                 275
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag   920
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu
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            280   285   290

ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa   968

Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys

295   300   305   310

gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg   1016

Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu

                315   320   325

aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata   1064

Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile

                330   335   340

ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg   1112

Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu

                345   350   355

gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag   1160

Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys

        360   365   370

aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat   1208

Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn

375   380   385   390

tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc   1256

Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe

                395   400   405

att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc   1304

Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala

            410   415   420

ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct   1352

Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala

           425   430   435

ttg aac ctt ctt ggc atc ctc cta cct gat gca aac agg gac aca ctg   1400

Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu

           440   445   450

aag gcc ctt ctt gaa ttt ctc caa aga gta ata gat aat aaa gaa aaa   1448

Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys

455   460   465   470

aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc   1496

Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu

              475   480   485

ttt atg tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa ttt   1544

Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe

            490   495   500

gta atg gca gct ggg aca gca aat acc atg cac tta ttg att aag tac   1592

Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr

           505   510   515

caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg   1640

Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg

           520   525   530

aag caa aac acg gaa aat cat aaa aag gat aaa aga gcc atg aag aaa   1688

Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys

535   540   545   550

ttg ctg aag aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat   1736

Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp

           555   560   565

aag agt aca aat gat gct gac gtt cct cag gga gtg att cga gtg caa   1784

Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln
             570   575   580

gct ccc cat ctt tcg aaa gtt tcc atg gca ata cag cta act gaa gaa   1832
Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu
             585   590   595

cta aaa gcc agt gat gta ctt gcc agg ttt ctc agc caa gaa agt ggg   1880
Leu Lys Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly
             600   605   610

gtt gcc cag act ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga   1928
Val Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly
615   620   625   630

gga aat att ggg gaa cgc tgc ctt gat gat gac act tac atg aag gat   1976
Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp
             635   640   645

tta tat cag ctt aac cca aat gct gag tgg gtt ata aag tca aag cca   2024
Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser Lys Pro
             650   655   660

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Leu

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aactcacgac ccaagttcat caatgttgaa taatatcacg tttaaataac aaaaaaatat 4057

ggactttaaa aaatctcaaa tttttttagag acagggtctt gctctgtttt ccagattgga 4117

gtgcagcagt gcattcgcgg ctaactgcag cctcaagcac tggggctcaa gcaaacctcc 4177

tgcctcagcc tcgtgagtag ctaggaccac aggtgcatgc caccatgcct ggctctaaag 4237

agaaaaaaaa cttgatacca tagagccttg aatataaata tcctgatgtt aacctactgc 4297

ttttgctgtg atttttttc cttagtgagt tttaaatctc aggctagatt tttatttgtt 4357

tttctgtgtg tgtatgagac aaaataaaaa taaatatatt tgccttgagt tt   4409

<210> 150

<211> 663

<212> PRT

<213> Homo sapiens

<400> 150

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Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala Lys Ala Gly
                20   25   30

Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln
            35   40   45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser
        50   55   60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile
65   70   75   80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln
                85   90   95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu
            100   105   110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly
        115   120   125

Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln
        130   135   140

Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
145   150   155   160

Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
                165   170   175

Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln
                180   185   190

Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala
                195   200   205

Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro
        210   215   220

Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
225   230   235   240

Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly
                245   250   255

Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly
                260   265   270

Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys
                275   280   285

His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile
        290   295   300

Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser Gly
305   310   315   320

Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys
                325   330   335

Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
            340   345   350

Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
            355   360   365

Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
            370   375   380

Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
385   390   395   400

Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser
                    405   410   415

Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
            420   425   430

Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp
            435   440   445

Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
            450   455   460

Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
465   470   475   480

Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
                    485   490   495

Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
            500   505   510

His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
            515   520   525

Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
            530   535   540

Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu

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        545                550                555                560
Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln
                     565                570                575
Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
                     580                585                590
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe
                     595                600                605
Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val
                     610                615                620
Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
        625                630                635                640
Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp
                     645                650                655
Val Ile Lys Ser Lys Pro Leu
                     660
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<210> 151

<211> 4490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3).. (2591)

<400> 151

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   Met Gly Tyr Ile Pro Ser Ser Tyr Val Gln Pro Leu Asn Tyr Arg
   1                5                10                15
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aac tca aca ctg agt gac agc ggt atg att gat aat ctt cca gac agc   95
Asn Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser
             20   25   30

cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat   143
Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp
             35   40   45

gac aaa aaa gta cca ggc aga atg tac agt aat aac cct ttc tgg aat   191
Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn
             50   55   60

ggg gtc cag acc aat cca ttt ctg aat ggg aac gtg ccc gtc atg ccc   239
Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro
             65   70   75

agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt   287
Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe
80   85   90   95

gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat   335
Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn
                     100   105   110

agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac   383
Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His
             115   120   125

gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc   431
Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
             130   135   140

tcc tac agt ctc tcg gaa ctc tcc gtc ctc caa gcc aag tcc gac gct   479
Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala

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                 145                  150                  155

ccc aca tcg tcg agt ttc ttc acc ggc ttg aaa tca cct gcc ccc gag    527
Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu

160                  165                  170                  175

caa ttt cag agc cgg gag gat ttt cga act gcc tgg cta aac cac agg    575
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg

                 180                  185                  190

aag ctg gcc cgg tct tgc cac gac ctg gac ttg ctt ggc caa agc cct    623
Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro

                 195                  200                  205

ggt tgg ggc cag acc caa gcc gtg gag aca aac atc gtg tgc aag ctg    671
Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu

                 210                  215                  220

gat agc tcc ggg ggt gct gtc cag ctt cct gac acc agc atc agc atc    719
Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile

                 225                  230                  235

cac gtg ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc    767
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser

240                  245                  250                  255

atg aaa gcc ctg ctg gac ccc ccg ctg gag ctc aac agt gac agg tcc    815
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser

                 260                  265                  270

tgc agc atc agc cct gtg ctg gag gtc aag ctg agc aac ctg gag gtg    863
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val

                 275                  280                  285

aaa acc tct atc atc ttg gag atg aaa gtg tca gcc gag ata aaa aat    911
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn
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                290   295   300

gac ctt ttt agc aaa agc aca gtg ggc ctc cag tgc ctg agg agc gac   959
Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp
           305   310   315

tcg aag gaa ggg cca tat gtc tcc gtc ccg ctc aac tgc agc tgt ggg   1007
Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly
320   325   330   335

gac acg gtc cag gca cag ctg cac aac ctg gag ccc tgt atg tac gtg   1055
Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val
                        340   345   350

gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg   1103
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp
           355   360   365

gac ttc atc aat aaa aaa gtc aca gtg ggt ctc tac ggc cct aaa cac   1151
Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His
           370   375   380

atc cac cca tcc ttc aag acg gta gtg acc att ttt ggg cat gac tgt   1199
Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys
           385   390   395

gcc cca aag acg ctc ctg gtc agc gag gtc aca cgc cag gca ccc aac   1247
Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn
400   405   410   415

cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttg   1295
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu
                        420   425   430

tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat   1343

Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn

        435   440   445

tac gag gtc aaa gcc agc gag cag gcc aaa gtg gtg cga gga ttc cag   1391

Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln

        450   455   460

ctg aag ctg ggc aag gtg agc cgc ctg atc ttc ccc atc acc tcc cag   1439

Leu Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln

        465   470   475

aac ccc aac gag ctc tct gac ttc acg ctg cgg gtt cag gtg aag gac   1487

Asn Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp

480   485   490   495

gac cag gag gcc atc ctc acc cag ttt tgt gtc cag act cct cag cca   1535

Asp Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro

          500   505   510

ccc cct aaa agt gcc atc aag cct tcc ggg caa agg agg ttt ctc aag   1583

Pro Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys

        515   520   525

aag aac gaa gtc ggg aaa atc atc ctg tcc ccg ttt gcc acc act aca   1631

Lys Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr

        530   535   540

aag tac ccg act ttc cag gac cgc ccg gtg tcc agc ctc aag ttt ggt   1679

Lys Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly

        545   550   555

aag ttg ctc aag act gtg gtg cgg cag aac aag aac cac tac ctg ctg   1727

Lys Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu

560   565   570   575

gag tac aag aag ggc gac ggg atc gcc ctg ctc agc gag gag cgg gtc   1775

Glu Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val
                    580   585   590

agg ctc cgg ggc cag ctg tgg acc aag gag tgg tac atc ggc tac tac   1823
Arg Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr
                595   600   605

cag ggc agg gtg ggc ctc gtg cac acc aag aac gtg ctg gtg gtc ggc   1871
Gln Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly
            610   615   620

agg gcc cgg ccc agc ctg tgc tcg ggc ccc gag ctg agc acc tcg gtg   1919
Arg Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val
        625   630   635

ctg ctg gag cag atc ctg cgg ccc tgc aaa ttc ctc acg tac atc tat   1967
Leu Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr
640   645   650   655

gcc tcc gtg agg acc ctg ctc atg gag aac atc agc agc tgg cgc tcc   2015
Ala Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser
                    660   665   670

ttc gct gac gcc ctg ggc tac gtg aac ctg ccg ctc acc ttt ttc tgc   2063
Phe Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys
                    675   680   685

cgg gca gag ctg gat agt gag ccc gag cgg gtg gcg tcc gtc ctg gaa   2111
Arg Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu
                690   695   700

aag ctg aag gag gac tgt aac aac act gag aac aaa gaa cgg aag tcc   2159
Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser
                705   710   715

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ttc cag aag gag ctt gtg atg gcc cta ctg aag atg gac tgc cag ggc      2207
Phe Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly
720             725                 730                 735

ctg gtg gtc aga ctc atc cag gac ttt gtg ctc ctg acc acg gct gta      2255
Leu Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val
                740                 745                 750

gag gtg gcc cag cgc tgg cgg gag ctg gct gag aag ctg gcc aag gtc      2303
Glu Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val
                755                 760                 765

tcc aag cag cag atg gac gcc tac gag tct ccc cac cgg gac agg aac      2351
Ser Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn
            770                 775                 780

ggg gtt gtg gac agc gag gcc atg tgg aag cct gcg tat gac ttc tta      2399
Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu
        785                 790                 795

ctc acc tgg agc cat cag atc ggg gac agc tac cgg gat gtc atc cag      2447
Leu Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln
800             805                 810                 815

gag ctg cac ctg ggc ctg gac aag atg aaa aac ccc atc acc aag cgc      2495
Glu Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg
                820                 825                 830

tgg aag cac ctc act ggg act ctg atc ttg gtg aac tcc ctg gac gtt      2543
Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val
                835                 840                 845

ctg aga gca gcc gcc ttc agc cct gcg gac cag gac gac ttc gtg att      2591
Leu Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
        850                 855                 860
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tgaatgggtc ccctcccctc ctgctgctct ggagtgcaag ccctcttctg ccctgcgtgc 2651

cctgctgtca ccgcggagct gaagagggag gaaggggcgg ctgctcagac agatttaggg 2711

cccgccagct aggctacacc catcatgcgc cgccctcctc catcgaggga gaggcctgaa 2771

gggactgcct actgcagctc gttgccaatc acatagcttt ctatttgtta agtataaatt 2831

taaatttaaa atcacttttt taacgaatgg ggggaaggga tctatgagaa aggtggtatc 2891

taattttttt atggaccata aaggtttaaa agaaaatagg ggcacagggt gttgaggttt 2951

ttatgttgtt atagaccttt ttaaattatg ttagagatgt atataggtat ttaaaggtca 3011

ctgggagcat ttctgattcc cggccacact ttgcatttca acactcagcc cggaaagatg 3071

ctcgttcggt tgttggacct ctttcactcc ctgcgtgtaa gaaggtgaat cacgtgggaa 3131

aaagtggctt ttcagtaaac gggtacagct cattctttct gagaaggccc caggtcctgc 3191

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gggcccctgc cagtgtgcaa ttagtcattg acaagaacaa tgccatttga gagtgaggtg 3431

gtccctgctg ctacgaggcc attgtactgt tttttccttg aggtcaaagc agtgcttccc 3491

atagagtttg ctgcctcttc tgtggacagg aagaaaactt catgaccgaa tcagagcctt 3551

ggtggccact gactctcgtg cttattgcag atgctgtggt tggcctcaca agcaacgcct 3611

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gggtgcagac atgctgtgtg aatctcacaa tgcgtcgtag atgtcgcgtg ttggaaggga 3911

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tcctcagggg ctttaaatag tttcctatgc aacgtgtctt gtagcacaaa taaaattcta 4391

caaaagttgc agtaaatttt atttggatat tttaacctgt taagtgtgtg tgtgttttct 4451

gtacccaacc agactttaaa taaaacaaac atgaaacct   4490

<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

Met Gly Tyr Ile Pro Ser Ser Tyr Val Gln Pro Leu Asn Tyr Arg Asn
1   5   10   15

Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser Pro
            20   25   30

Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp
        35   40   45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly
    50   55   60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser
65   70   75   80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp
                85   90   95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser
            100   105   110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

```
                115                  120                  125
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser
            130            135                140
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro
145                150                155                160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln
                165                  170                  175
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys
            180            185                190
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly
                195                  200                  205
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp
            210            215                220
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His
225                230                235                240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met
                245                  250                  255
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys
            260            265                270
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys
            275            280                285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp
        290                295            300
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser
305                310                315                320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp
                325                  330                  335
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Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala
            340   345   350

Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
            355   360   365

Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile
        370   375   380

His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala
385   390   395   400

Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro
                    405   410   415

Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser
            420   425   430

Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr
            435   440   445

Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu
        450   455   460

Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn
465   470   475   480

Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp
                    485   490   495

Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro
            500   505   510

Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys
            515   520   525

Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys
        530   535   540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys
545   550   555   560

Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu
                    565   570   575

Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg
                    580   585   590

Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln
                    595   600   605

Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg
                    610   615   620

Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu
625   630   635   640

Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala
                    645   650   655

Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe
                    660   665   670

Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg
                    675   680   685

Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys
                    690   695   700

Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe
705   710   715   720

Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu
                    725   730   735

Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu
                    740   745   750

Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

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            755                  760                  765
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly
           770                  775                  780
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu
785                  790                  795                  800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu
                    805                  810                  815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp
           820                  825                  830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu
           835                  840                  845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile
           850                  855                  860
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<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1125)

<400> 153

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ggtgcggcgc tggtcccctc agagggttcc tgctgctgcc ggtgccttgg accctccccc 60

tcgcttctcg ttctactgcc ccaggagccc ggcgggtccg ggactcccgt ccgtgccggt 120

gcgggcgccg gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171
              Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro
              1               5                  10
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ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc   219
Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val
        15   20   25

aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc   267
Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe
30   35   40   45

agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc   315
Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro
                50   55   60

cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg   363
Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala
                65   70   75

ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca   411
Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala
                80   85   90

aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc   459
Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val
        95   100   105

tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga   507
Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg
110   115   120   125

ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca   555
Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala
                130   135   140

aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta   603
Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu

                    145   150   155

agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt   651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe
              160   165   170

gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg   699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met
              175   180   185

tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc   747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe
190   195   200   205

ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata   795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile
              210   215   220

aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg   843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly
              225   230   235

aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg   891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met
              240   245   250

gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt   939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys
              255   260   265

gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac   987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr
270   275   280   285

ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt   1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val

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                  290                 295                 300
aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc agc   1083
Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser

                          305                 310                 315
tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc          1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

                  320                 325                 330
tagactttca cggtgggacg aaacgggttc agaaactgcc aggggcctca tacagggata 1185

tcaaaatacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac acaaatgcaa 1245

tagttggtca ctgcattttt acctgaacca aagctaaacc cggtgttgcc accatgcacc 1305

atggcatgcc agagttcaac actgttgctc ttgaaaatct gggtctgaaa aaacgcacaa 1365

gagcccctgc cctgccctag ctgaggcaca cagggagacc cagtgaggat aagcacagat 1425

tgaattgtac agtttgcaga tgcagatgta aatgcatggg acatgcatga taactcagag 1485

ttgacatttt aaaacttgcc acacttattt caaatatttg tactcagcta tgttaacatg 1545

tactgtagac atcaaacttg tggccatact aataaaatta ttaaaaggag cactaaagga 1605

aaactgtgtg ccaagcatca tatcctaagg catacggaat ttggggaagc caccatgcaa 1665

tccagtgagg cttcagtgta cagcaaccaa aatggtaggg aggtcttgaa gccaatgagg 1725

gatttatagc atcttgaata gagagctgca aaccaccagg gggcagagtt gcattttttcc 1785

aggcttttta ggaagctctg caacagatgt gatctgatca taggcaatta gaactggaag 1845

aaacttccaa aaatatctag gtttgtcctc attttacaaa tgaggaaact aaactctgtg 1905

gaagggaagg ggttgcctca aaagtcacag cttagctggg cacagtggct catgccgata 1965

atcccagcaa ttcagaaagc tgaggcagga ggattacttg aggccagact gggcaatata 2025

gcaagacccc atctctaaaa aattaggcat ggtggtgcat gcctgtattc ccagctactc 2085

aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccatga 2145

ttacaccacg gcactacaac cttggtggca cagtgagaac ctgactctt            2194
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<210> 154

<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
                20   25   30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
        35   40   45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
        50   55   60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
65   70   75   80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
                85   90   95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
                100   105   110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
            115   120   125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
        130   135   140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala
145   150   155   160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
                165   170   175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
            180   185   190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
            195   200   205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
            210   215   220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
225   230   235   240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
            245   250   255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
            260   265   270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
            275   280   285

Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
            290   295   300

Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
305   310   315   320

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
            325   330

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

⟨222⟩ (44)..(1666)

⟨400⟩ 155

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                                                   Met Leu Ser Pro

                                                    1

cag cga gtg gga gca gct gcc tca aga gga gca gat gat gcc atg gag   103

Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu

 5   10   15   20

agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa   151

Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln

                 25   30   35

cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag   199

His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln

             40   45   50

gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc   247

Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala

         55   60   65

ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta   295

Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu

     70   75   80

tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa   343

Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu

 85   90   95   100

gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc   391

Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr

                 105   110   115

act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt   439

Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
        120   125   130

ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac   487
Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp
        135   140   145

agc cag tca act gtg aaa gac tgt gct acc atc ttt gct cta agc act   535
Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
    150   155   160

atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa   583
Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
165   170   175   180

gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca   631
Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
            185   190   195

atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt   679
Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
        200   205   210

aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga   727
Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
        215   220   225

atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa   775
Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu
    230   235   240

gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc   823
Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val
245   250   255   260

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acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct      871
Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro
             265                 270                 275

gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag      919
Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln
             280                 285                 290

tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa      967
Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu
         295                 300                 305

aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat     1015
Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr
     310                 315                 320

ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc     1063
Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro
325             330                 335                 340

aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca     1111
Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala
                 345                 350                 355

gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg     1159
Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly
                 360                 365                 370

gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt     1207
Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys
             375                 380                 385

gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg     1255
Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met
     390                 395                 400
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ggt ggg aag gat ttc agc ttt cgt tac cag cag gag ctg gag gag gaa   1303
Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu
405   410   415   420

atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac   1351
Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn
                    425   430   435

gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta   1399
Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe Thr Gly Ile Val
                440   445   450

gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt   1447
Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val
            455   460   465

gta gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc   1495
Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Leu Ile Ala Leu
            470   475   480

ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc   1543
Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
485   490   495   500

gga gct att gat ttt ggt gcc gca tat gtg ttg gag cag gct tct tct   1591
Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
                    505   510   515

cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga   1639
His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
                    520   525   530

aga cca tcc atg gat aaa aaa gct caa tagcatctta acgtgaagat   1686
Arg Pro Ser Met Asp Lys Lys Ala Gln

535   540

caaacaagaa cacaacaagc ccctactgat ttctgggttt ctgccacggc cacaggttca 1746

tatccagagg aatggcagat ctgagacgat ccaggaagag ctaaaacatg gccctgtaat 1806

aaatgagcag acctctcctg tggtttcaaa ttattaaaca cacttccatt tctcttggaa 1866

gcatttcttt tccttgctgt tatagatgca agcctgtgtc tattttcata ttactctgct 1926

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tatgtgccac ttagtgcctt ttaagattga ttccatggtt ttgcacacac gatggggagg 2046

ggatggagga taacctcatg aaaggtgcca ttttcgggtg aaacttgaca tttctttat 2106

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agccaccgtg cccggccaag aaggattcct tttttaaaag tttacagaac ttggagaaac 2466

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gaatcctgtt gccacatagt gtggaaaaat catgtcatat ttaaatatac catactctga 2586

aatgtgaggt ttttacccag taggctgaca gttttgttgc aacttgctct attttttttt 2646

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gtggctcata ataaaaggaa tgcgctagat acttcaagaa aaaagctaag tttaaatgaa 2766

ccatgtgacc tctgataagt cacttgaact tgtgccttag tcaggttcac tgtaggttta 2826

catatgtatg tatgttttac acaactcttg taattgtcat ttgaggggtt cacttcctcc 2886

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tttgctctca aggtgtttga ggctttaatg caacccttta gcccttggtt cttttttggtg 3006

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ttttttctgt acataactgt gttctcagag ctgaatgttt atatcttttg ctgtgcaaaa 3306

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<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

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1               5                   10                  15

Asp Ala Met Glu Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val
            20                  25                  30

Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser
        35                  40                  45

Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser
    50                  55                  60

Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met
65                  70                  75                  80

Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu
                85                  90                  95

Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser
                100                 105                 110

Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val
        115                 120                 125

Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln
    130                 135                 140
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Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe

145   150   155   160

Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln

                165   170   175

Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr

                180   185   190

Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu

                195   200   205

Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly

        210   215   220

Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu

225   230   235   240

His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys

                245   250   255

Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val

                260   265   270

Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu

                275   280   285

Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser

        290   295   300

Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly

305   310   315   320

Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp

                325   330   335

Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn

        340   345   350

Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu
        355   360   365

Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu
        370   375   380

Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys
385   390   395   400

Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu
                405   410   415

Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn
                420   425   430

Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe
        435   440   445

Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile
        450   455   460

Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu
465   470   475   480

Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr
                485   490   495

Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu
                500   505   510

Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp
        515   520   525

Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln
        530   535   540

⟨210⟩ 157

⟨211⟩ 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)..(563)

<400> 157

ggaacacggc acccgcactg cgcgtcatgg tgcaggcctg gtat atg gac gac gcc   56

                                                   Met Asp Asp Ala
                                                    1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg   104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

 5   10   15   20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat   152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

                  25   30   35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag   200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

           40   45   50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta   248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

           55   60   65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac   296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

           70   75   80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat   344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85   90   95   100

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gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga     392
Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly
                105                 110                 115
gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac     440
Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp
                120                 125                 130
gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg     488
Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val
            135                 140                 145
tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag     536
Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln
        150                 155                 160
tac gtg aaa ttt ctg gca cag acc gcc tagcagtgct gcctgggaac          583
Tyr Val Lys Phe Leu Ala Gln Thr Ala
165                 170
taacacgtgc ctcgtaaagg tccccaatgt aatgactgag cagaaaatca atcactttct 643
ctttgctttt agaggatagc cttgaggcta gattatcttt cctttgtaag attatttgat 703
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attttctgta actcaatcaa gactggtggg tccatggccc tgtgttagtt catgcattca 823
gttgagtccc aaatgaaagt ttcatctccc gaaatgcagt tccttagatg cccatctgga 883
cgtgatgccg cgcctgccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943
gaagacactt ttttctccaa aatgatgcct tggggtgggg agtggtaggg ggaagagctc 1003
ccaccctaag gggcacacac tgagttgctt atgccacttc cttgttcaaa ataaagtaac 1063
tgccttaatc ttatactcat ggcttggagt taccttatat tcaggtatat gtgatatttt 1123
gcctggtttg ttaaaattgc cccatttaga ttccttctat aattgttctt atagataagt 1183
aatttatata tgagctgtgt tagtattttt tcagtgtgag atctctggat tctttcacaa 1243
```

```
taaagctgtt gaattttaac aggagtatta gtacataaat tttctactca acaattccga 1303

gataggatta tgcctagttt gtcatatcac agaaaaactc caagttaact tcatgttttg 1363

gaagggcagg tcgtttttaa agtatttctt tttttaactg gatgaaaaat cttcatgtta 1423

ggattaattt tcttaatcac ctccacactg tacagaggaa actcaagcct taaatgttta 1483

agtaaactct gtctcagttt taggattaaa atacccaccg gtggtgtgat gatgccatat 1543

accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaat aagtgctgat 1603

ctactgattt tttttaatgg attcatttct aaatgggcat tataaataga gcttgttcat 1663

ttttaagaac gaaacattca tatgataaac tatcgcttta aattgccttt cttgcttcat 1723

ataacttttc cctgtcagga tccttagtgt ttgaaactcc tcgtgcgggg ctggcctcct 1783

gcggactcta gtttcgcctc cttgatgtgg cgcctgggat ttcttcactt cagagctgta 1843

ttttttacagg caagagtaag ttcctgggca cagtggctca tgcctgtaat ctcagctact 1903

caggaggcta aggtgggagg attcttagag cctgggaggt cgaggctgca gtgagctgtg 1963

attgtggcca ctgcactcca gcctgggtga cagagcgaga ctctgtctca aaaaagaaga 2023

aagagtaaga gctgaggcat ataatagaat tctgctaaag cacttaaggt gaaatcacat 2083

tttcttttcc caggatgttg ctcacatctt tcgttttat tgaggtgtca tttatgtaca 2143

ataaaatgta ctcattttca gtgtttttg                                    2172
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<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

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Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro
1               5                   10                  15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr
            20                  25                  30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys
```

```
              35                   40                   45
```

Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys

```
              50                   55                   60
```

Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu

```
  65                   70                   75                   80
```

Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser

```
                   85                   90                   95
```

Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe

```
                   100                  105                  110
```

Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg

```
              115                  120                  125
```

Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val

```
              130                  135                  140
```

Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu

```
  145                  150                  155                  160
```

Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala

```
                   165                  170
```

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgtta cttctgctct   20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtctcg agtttttttt ttttttttt   50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c   41

<210> 162
<211> 30
<212> RNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence
<400> 162
agcaucgagu cggccuuguu ggccuacugg   30

<210> 163
<211> 42
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized oligo(dT)primer sequence
<400> 163
gcggctgaag acggcctatg tggcctttttt ttttttttt tt   42

<210> 164
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 164
agcatcgagt cggccttgtt g   21

<210> 165
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 165
gcggctgaag acggcctatg t   21

<210> 166
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 166
actttattgt catagtttag atctattttg   30

<210> 167
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence: an artificially synthesized primer
sequence
<400> 167
ataatcctta aaaactccat ttccacccct   30

<210> 168
<211> 1536
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (139).. (1062)
<400> 168
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCGCG CTCGTACTGG   60
 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GGCGGCCACG GCAGGATTAA   120
 CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC   171
                     Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
                      1   5   10

```
TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT        219
Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp
            15              20                  25

GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG        267
Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg
            30              35                  40

TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT        315
Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe
            45              50                  55

TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT        363
Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala
  60              65                  70                  75

TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC        411
Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe
                80                  85                  90

AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC        459
Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly
            95                  100                 105

GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC        507
Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His
            110             115                 120

AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC        555
Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp
            125             130                 135

ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG        603
Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met
140             145                 150                 155

CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC        651
Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly
                160             165                 170

CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG        699
Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg
                175             180             185

CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT        747
Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn
                190             195                 200

TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA        795
Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val
            205             210                 215
```

```
ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA          843
Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys
220                 225             230                 235

GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA          891
Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys
                    240             245                 250

ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT          939
Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu
                255             260             265

TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC          987
Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala
            270             275             280

ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC         1035
Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly
            285             290             295

AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA      1089
Ser Leu Gly Ile Ser Gln Glu Glu Gln
300                 305

GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC      1149
TTCAGGTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC      1209
TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAACTGT TCCCTCTTTG GTTTTCTTAG      1269
CTTTTGAATT TGAAGAAGTA CTTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC      1329
TACCAAAAGT CTTCACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT      1389
TGTGGTGGTT TTTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTTCTTTTT ATGTTGTTTG      1449
CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTTCTTGG  1509
ATATAACCAT GATCAGAGTG CCATGGC                                         1536
```

<210> 169
<211> 308
<212> PRT
<213> Homo sapiens
<400> 169

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Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
1               5                   10                  15
Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp
            20              25                  30
Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
        35              40                  45
Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
        50              55                  60
Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
65                  70                  75                  80
Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
                85                  90                  95
His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
                100                 105                 110
Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val
```

```
                 115                    120                    125
    His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
         130                    135                    140
    Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
    145                    150                    155                    160
    Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
                     165                    170                    175
    Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly
                     180                    185                    190
    Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr
                     195                    200                    205
    Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val
         210                    215                    220
    Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys
    225                    230                    235                    240
    Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe
                     245                    250                    255
    Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His
                     260                    265                    270
    Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met
                     275                    280                    285
    Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser
         290                    295                    300
    Gln Glu Glu Gln
    305
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<210> 170
<211> 2560
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
(202).. (1002)
<400> 170
CTGGCCTACT GGGGCTCCAG CCGTGTCCTG AGGAGCTGGA CCAGCCACAT CCCCTGGGGC      60
TGCAGTTGAA GCAGAACCAA GTGGCCATCC CGGCGTTAGA CCGTAGGTTC CTGGTCCCGG     120
AGTGGTCGGA GCCCGCCAGT GGGCAGGCAG CTCTTGCTCA CAGGCCGCGG TGCCCAGGCC     180
GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC      231
                       Met Ala Leu Gln Val Glu Leu Val Pro Thr
                        1               5                   10


GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC      279
Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala
                15                    20                    25


CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC      327
Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala
            30                    35                    40


CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC      375
Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr
            45                    50                    55
```

```
AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT        423
Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn
     60                      65                  70

CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC        471
Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr
 75                      80                  85                  90

CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC        519
Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly
                 95                 100                 105

GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT        567
Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr
             110                 115                 120

GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC        615
Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile
         125                 130                 135

TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG        663
Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu
     140                 145                 150

CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG        711
Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val
155                 160                 165                 170

CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT        759
Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn
                 175                 180                 185

GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG        807
Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met
             190                 195                 200

GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC        855
Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu
             205                 210                 215

AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG        903
Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu
             220                 225                 230

CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA        951
Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg
235                 240                 245                 250

CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC        999
Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr
             255                 260                 265

TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTCG       1058
```

Trp

```
TCAGGAAGGC TCTGACAGTC ATTGATTTCA CCGAGGATGA AGTGGAGGAC CTGCTGAGCA      1118
TCGTGGCCAG CGTCCTTCAT TTGGGCAACA TCCACTTTGC TGCCAACGAG GAGAGCAATG      1178
CCCAGGTCAC CACCGAGAAC CAGCTCAAGT ATCTGAGCCC ATTCAGTATG CGGTGCCTGT      1238
TGTGAAATAC GACCGCAAGG GCTACAAGCC TCGCTCCCGG CAGCTGCTGC TCACGCCCAA      1298
CGCCGTCGTC ATCGTGGAGG ACGCCAAAGT CAAGCAGAGG ATTGATTACG CCAACCTGAC      1358
CGGAATCTCT GTCAGCAGCC TGAGCGACAG TCTTTTTGTG CTTCATGTAC AGCGTGCGGA      1418
CAATAAGCAA AAGGGAGATG TGGTGCTGCA GAGTGACCAC GTGATTGAGA CGCTGACCAA      1478
GACAGCCCTC AGTGCCAACC GCGTGAACAG CATCAACATC AACCAGGGCA GCATCACGTT      1538
TGCAGGGGGC CCCGGCAGGG ATGGCACCAT TGACTTCACA CCCCGGCTCGG AGCTGCTCAT      1598
CACCAAGGCC AAGAACGGGC ACCTGGCTGT GGTCGCCCCA CGGCTGAATT CTCGGTGATA      1658
AAGGCGCCCA CTGGACCCTC CCAACGCCCA ATGCTTTGCT TTTCTCCTCC TCCCCTTCCC      1718
AGTTACCAAA GACTCGAACT TCCAGACAGG GACCCAGGGA CACCCCGAAG CCCACCTGCA      1778
ATCTCCCACC TCCTGCCCAT CCCTCTCTTG AGGGAGCAGC AGGGGCCAGG AGCTACCCCA      1838
GGAGTGGGCC AGGCCGGGCC ACAGCAATAG GAAAGCCAGG GCCAGAGCGA GCCATGCCAG      1898
CCCTACTGCC GATGCCAAAT ATTTGAGAGA AGGGAACTTT TGCTGAGGTT TTCTCTGAGG      1958
TTTTTTTTGA TGCTTTATAG GAAACTATTT TTTAAAAAAA GCCATTTCCC ACCCAAGGAC      2018
ACAGTGGATG TGTTTTCCCT GACTCCAGCA GGGCAAGGAA ATGTAGCCGA GAGGTTGTGT      2078
GGGCTGGGCT CTGGTGCCCT CTTCCCTGGC CAGGACACCT CTCCTCCTGA TTCCCTTGGC      2138
ACCTTGTCTT TCTGTCTGTT TACCTGTCTC CCTGCCTGCC CATCTGCATC TTTTGCAGCC      2198
CACTCTGACT TCCATCTGGG GGCTGAGACC ACCCTTGCCT GCCCCCTTCT TTCTGCCTTA      2258
AGAATGTCCT TTTAGGCTGG GCATGGTGGC TCACGCCTGT AACCCCAGCA CTTTGGGAGG      2318
CGGAGACGGG CAGATAACCT GAGGTCAGGA TTTCGAGACC AACCTGACCT ACATGGAGAA      2378
ACTCCGCCTC TGGTAAGGAT ACAAAATTAG CCGGGCATGG TGGTGCACGC CTCTAATCCC      2438
AGCTGCTCGG GAGGCTGAGG CAGGAGAATC ACTTGAACCC GGGAAGTGGA GGTTGCAGTG      2498
AGCCAAGAGT ACACCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTCC GTCTTAAAAA      2558
AA                                                                    2560
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<210> 171
<211> 267
<212> PRT
<213> Homo sapiens
<400> 171

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Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val
1               5                   10                  15
Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val
                20                  25                  30
Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val
        35                  40                  45
Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile
    50                  55                  60
Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile
65                  70                  75                  80
Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr
                85                  90                  95
Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val
            100                 105                 110
Pro Pro His Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg
        115                 120                 125
Thr Glu Arg Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala
    130                 135                 140
Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr
```

```
          145                 150                    155                    160
          Cys Pro Ala Pro Glu Arg Gly Gly Ala Val Arg Asp Arg Leu Leu Gln
                          165              170              175
          Ser Asn Pro Val Leu Glu Ala Phe Gly Asn Ala Lys Thr Leu Arg Asn
                      180                  185              190
          Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met Asp Val Gln Phe Asp Phe
                      195                  200              205
          Lys Gly Ala Pro Val Gly Gly His Ile Leu Ser Tyr Pro Leu Glu Lys
                  210                  215              220
          Ser Arg Val Val His Gln Asn His Gly Glu Arg Asn Phe Thr Ser Ser
          225                  230                  235              240
          Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg Leu Phe Ala Gly Trp Ala
                          245                  250                  255
          Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr Trp
                          260                  265
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<210> 172
<211> 2650
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (116)..(1216)
<400> 172

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CTTTTGCTGC TGCGCCCGGG CAGGGGCTGC CGCGGCCCCA GGTCCCGCTT CGAGACGCGG          60
CGCGGTCCAG GCGGGAGGCG ACTCCCTAGG AAGGGACCCG GGGCGGGAGG AGGAA ATG         118
                                                                  Met
                                                                   1


AGG CCG CGC GGA AGG AAG GCG GCG AGC CCC GGG GCC CCG AGG CCT TGG          166
Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp
                5                   10                  15


CCG CGT CAC AGC ACC CAC ATG GCC TCT GGA GTG GGC GCG GCC TTC GAG          214
Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu
            20                  25                  30


GAA CTG CCT CAC GAC GGC ACG TGT GAC GAG TGC GAG CCC GAC GAG GCT          262
Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala
        35                  40                  45


CCG GGG GCC GAG GAA GTG TGC CGA GAA TGC GGC TTC TGC TAC TGC CGC          310
Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg
    50                  55                  60                  65


CGC CAT GCC GAG GCG CAC AGG CAG AAG TTC CTC AGT CAC CAT CTG GCC          358
Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala
                70                  75                  80


GAA TAC GTC CAC GGC TCC CAG GCC TGG ACC CCG CCA GCT GAC GGA GAG          406
Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu
                85                  90                  95
```

```
GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG            454
Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu
        100             105             110

ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG            502
Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu
        115             120             125

TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT            550
Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp
130             135             140             145

GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA            598
Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu
                150             155             160

AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG            646
Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu
                165             170             175

GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA            694
Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu
        180             185             190

GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG            742
Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu
        195             200             205

AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA            790
Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro
210             215             220             225

GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC            838
Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala
                230             235             240

TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG            886
Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met
                245             250             255

ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA            934
Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val
                260             265             270

ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT            982
Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val
        275             280             285

CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC           1030
Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp
290             295             300             305

ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC           1078
```

```
Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp
            310                 315                 320
```

```
ATC CAA TCC CAC ATG GAT AGG TTG ATG ACT CAG ATG GCC CAA GCC AAG      1126
Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys
            325                 330                 335
```

```
GAA CAA CTT GAT ACC TCT AAT GAA TCA GCT GAG CCA AAG GCA GAG GGC      1174
Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly
            340                 345                 350
```

```
GAT GAG GAA GGA CCC AGT GGT GCC AGT GAA GAA GAG GAC ACA TGAAGGCTT    1225
Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
        355                 360                 365
```

```
GCTACCCCCA GTGGAAAATC ATCCCCTCCC CTTGTGTGTA TGTGACAGCG TGTATGTAAC    1285
GGCTTCTGAT TTCTGTGAAA GCTGCTCAGC AACAAACGTA CTTCCACCAG ATGTGTCCCC    1345
AGATCCACAG CAGGCACATA TCTCTCCAAG GGATGACCAG TTTTATGCTT ACTGTGTGCT    1405
TCTCATCCCC TGGTTGTGGT AGGTCAAGGA AAAGAGCCCC TTTGATCCAC CAGGAGCAAT    1465
TAAGAAAGGT CCTTCAGGTA ATCCCTCAAT GGCTGCTTTG AACTTACTCA GGAAAGCCAG    1525
CCCCCATAAT ATTGTATTAC CAAACAGTAT CGCTTTGTTA GGAAGGATCT GGAATAATCT    1585
TGAAGGGAAG TCAGAGTTTT CTCCCTGCCT ATTAACAAAA ACCCAATTTT GTTCATATTG    1645
AAGCATGAAA TAAATGAGAG CAAGGTAGGG CCAAATTAAC TCTTGTGGAC AGTCCCTAAA    1705
AGTCCAGTTC TACATTGTG AAAATTGTGG TGCCATGAAT TAAGATGGAT GACTGGAAAA     1765
AGGTGTTGGA GAAAGAGTTA AAGATGAGGA AGAGATATTT TTAGTATATG AAGTTATCCA    1825
GGACTTGATA TTCATAATTC AGTGCTGTGG AAATGAAAAA AATGATTGAA GAGGTGGAAC    1885
GGAAATGACC TTAGGGGGAA AAAAAAGGAC CAAAGAAGTC TGATTAAAAG TTGAAATCAG    1945
TATTTCTGAA TTCAAATTGC TTGAATTTCC AAAATAGTCA GTAAAGGATC TAATAGAACC    2005
AGAATTATTT GGGTGAATTC TGCAGGTTTT ATGGGCTTGT CACAACGTGA AGGGCTGGAA    2065
TGTATATTAC CAAATGGGAA TTTCCATTGT AGGTTTTTGC TAGTCCCACC CCCATTTTAG    2125
CCTAATTTGG CTTAAACGCA GTATGGGGAG AATTGTTCCC ATTCCATGTG TTCTGAATTC    2185
AGCTCATCTC CCAGCATATA GATATATCCT CCTTTAACTC CGACCAGAAC CCTTCTTCCT    2245
GTGGCACTCC CCACCCATAG ACCTTCAGAT CATCTCCCAC ACCCTGGATC TCACTCTCCT    2305
CTTAGTAACA GAGACACTCC TGAGGTTGGA CTTCCTTGCT TTTCTCTACT TCCAAATCAC    2365
AATTTCTTAC AACCAAGCTT TGTGCTCCCG AGTAAGCAGG GATGTACTAG GGGAATGTAA    2425
AACTGCAAAC TTAAAAACCT GCATCTTCTT GAAGCATCAG TTTTACTTAC CAAATGGTTT    2485
AGAGTCATAA GATGACCTAT TTTTATATAA AAGTTATATT ATAGAATAAA ATGTTCATAC    2545
GCATAGACTG TTAAG                                                    2560
```

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<210> 173
<211> 367
<212> PRT
<213> Homo sapiens
173
Met Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro
  1               5                 10                  15
Trp Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe
            20                  25                  30
Glu Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu
            35                  40                  45
Ala Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys
            50                  55                  60
Arg Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu
```

```
            65                    70                    75                    80
Ala Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly
                    85                    90                    95
Glu Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg
                    100                   105                   110
Glu Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser
                    115                   120                   125
Glu Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser
                    130                   135                   140
Asp Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln
145                   150                   155                   160
Glu Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala
                    165                   170                   175
Glu Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met
                    180                   185                   190
Glu Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp
                    195                   200                   205
Leu Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys
                    210                   215                   220
Pro Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu
225                   230                   235                   240
Ala Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala
                    245                   250                   255
Met Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys
                    260                   265                   270
Val Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys
                    275                   280                   285
Val Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val
                    290                   295                   300
Asp Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala
305                   310                   315                   320
Asp Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala
                    325                   330                   335
Lys Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu
                    340                   345                   350
Gly Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
                    355                   360                   365
```

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<210> 174
<211> 41
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 174
ttaagcttgc caccatgagc aacccagcg ccccaccacc a                    41

<210> 175
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
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<223> Description of the artificial sequence:a synthetic DNA

<400> 175
gtatcgattt aattgcgatc ccccatcag   29

176
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 176
cacctactgtatgacaccacattc   24

<210> 177
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 177
gagatgctgttccatgctggcctg   24

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 178
ggaaagctctccgtggctaacaag   24

<210> 179
<211> 24 .
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 179
catagtccttgacaagggtcacag   24

<210> 180
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc   22

<210> 181
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of the artificial sequence:a synthetic DNA

<400> 181
ttcaccaccttcttgatgtcatcata   26

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

A. CLASSIFICATION OF SUBJECT MATTER
Int.Cl⁷   C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int.Cl⁷   C12N15/11-15/62, C07K14/00-14/825

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
GenBank/EMBL/DDBJ/GeneSeq,SwissProt/PIR/GeneSeq,
BIOSIS(DIALOG),WPI(DIALOG)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 99/14327, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, PRO246, FIG.26 (Accession No.X28436), FIG.27 (Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2,4,11,12, 36-40,43, 45,46
X	WO, 99/14328, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, FIGURE 16 (Accessiion No.X52221), FIGURE 17 (Accession No.Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	2,4,11,12, 36-40,43, 45,46
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.), 24 August, 1999 (24.08.99), especially, SEQ ID NO:2 (Accession No.X87000), SEQ ID NO:1 (Accession No.Y27096) (Family: none)	2,4,11,12, 36-40,43, 45,46
P,X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.), 18 November, 1999 (18.11.99),	2,4,11,12, 36-40,43,

☒ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier document but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
19 December, 2000 (19.12.00)	26 December, 2000 (26.12.00)

Name and mailing address of the ISA/	Authorized officer
Japanese Patent Office	
Facsimile No.	Telephone No.

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	especially, SEQ ID NO:39 (Accession No.Z65278), SEQ ID NO:291 (Accession No.Y76303) & AU, 9938831, A	45,46
P,X	WO, 00/11015, A1 (ALPHAGENE, INC.), 02 March, 2000 (02.03.00), especially, SEQ ID NO:37 (Accession No.A23441), SEQ ID NO:38 (Accession No.Y94999) & AU, 9957847, A	2,4,11,12, 36-40,43, 45,46
P,X	WO, 00/15666, A2 (GENENTECH, INC.), 23 March, 2000 (23.03.00), especially, FIGURE 15 (Accession No.A30052), FIGURE 16 (Accession No.Y88574) & AU, 9958167, A	2,4,11,12, 36-40,43, 45,46
A	TOPPER, James N. et al., "Blood flow and vascular gene expression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1,2,4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Expression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1,2,4-12, 35-50

Box I   Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 22,33,51,57,66,69,76
   because they relate to subject matter not required to be searched by this Authority, namely:

   The inventions as set forth in claims 22, 33, 66 and 69 relate to "methods for inhibiting, promoting or controlling cell apoptosis". As stated in the description, these methods are performed for therapy in the human body. Therefore, these inventions pertain to methods for treatment of the human body by therapy. The inventions as set forth in claims 51, 57 and 76 relate to "drug delivery methods for inducing a fused antibody comprising an antibody bonded to a drug into arteriosclerotic focus" which are to be performed in the human body in therapy. Therefore, these inventions pertain to methods for treatment of the human body by therapy.

2. ☐ Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II   Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

   See extra sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

   The inventions as set forth in claims which relate to the base sequence represented by SEQ ID NO:143 or the amino acid sequence represented by SEQ ID NO:144

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

第Ⅰ欄１．の続き

薬剤とを結合させた融合抗体を動脈硬化巣へ誘導するドラッグデリバリー法」に関するもの
であり、ヒトを治療する際に体内で実施されるものであるから、人の身体の治療による処置
方法に該当する。

第Ⅱ欄の続き

，１１７，１１９，１２１，１２３，１２５，１２７，１３５，１３７，１３９，１４１，
１，３，５，７，９，１１，１３，１５，１７，１９，２１，２３，２５，２７，２９，３
１，３３，３５，３７，３９，４１，４３，４５，４７，４９，５１，５３，５５，５７，
５９，６１，６３，６５，６７，６９，７１，７３，７５，７７，７９，８１，８３，８
５，８７，８９，９１，９３，９５，９７，９９，１０１，１０３，１０５，１０７，１０
９で表される塩基配列（若しくは、配列番号１４４，１４６，１４８，１５０，１５２，１
５４，１５６，１５８，１６９，１７１，１７３，１１２，１１４，１１８，１２０，１２
２，１２４，１２６，１２８，１３６，１３８，１４０，１４２，２，４，６，８，１０，
１２，１４，１６，１８，２０，２２，２４，２６，２８，３０，３２，３４，３６，３
８，４０，４２，４４，４６，４８，５０，５２，５４，５６，５８，６０，６２，６４，
６６，６８，７０，７２，７４，７６，７８，８０，８２，８４，８６，８８，９０，９
２，９４，９６，９８，１００，１０２，１０４，１０６，１０８，１１０で表されるアミ
ノ酸配列）、又は、配列番号１１５，１１６，１２９，１３０，１３１，１３２，１３３，
１３４で表される塩基配列、のそれぞれに関連した発明に共通する事項は、「血管内皮細胞
においてずり応力刺激により発現が誘導されるＤＮＡ」ということである。しかしながら、
「血管内皮細胞においてずり応力刺激により発現が誘導されるＤＮＡ」としては、出願人も
認識しているように endothelin-1 や monocyte chemotactic protein-1 などが既に公知で
あったから、請求の範囲に記載された上記各塩基配列（又は、アミノ酸配列）に関連した発
明に共通する「特別な技術的特徴」は存在しないといえる。
　　したがって、請求の範囲には、配列番号１４３，１４５，１４７，１４９，１５１，１５
３，１５５，１５７，１６８，１７０，１７２，１１１、１１３，１１７，１１９，１２
１，１２３，１２５，１２７，１３５，１３７，１３９，１４１，１，３，５，７，９，１
１，１３，１５，１７，１９，２１，２３，２５，２７，２９，３１，３３，３５，３７，
３９，４１，４３，４５，４７，４９，５１，５３，５５，５７，５９，６１，６３，６
５，６７，６９，７１，７３，７５，７７，７９，８１，８３，８５，８７，８９，９１，
９３，９５，９７，９９，１０１，１０３，１０５，１０７，１０９で表される塩基配列
（若しくは、配列番号１４４，１４６，１４８，１５０，１５２，１５４，１５６，１５
８，１６９，１７１，１７３，１１２，１１４，１１８，１２０，１２２，１２４，１２
６，１２８，１３６，１３８，１４０，１４２，２，４，６，８，１０，１２，１４，１
６，１８，２０，２２，２４，２６，２８，３０，３２，３４，３６，３８，４０，４２，
４４，４６，４８，５０，５２，５４，５６，５８，６０，６２，６４，６６，６８，７
０，７２，７４，７６，７８，８０，８２，８４，８６，８８，９０，９２，９４，９６，
９８，１００，１０２，１０４，１０６，１０８，１１０で表されるアミノ酸配列）、又
は、配列番号１１５，１１６，１２９，１３０，１３１，１３２，１３３，１３４で表され
る塩基配列、のそれぞれに関連した別異の８６発明が包含されている。

INTERNATIONAL SEARCH REPORT

Continuation of Box No.II of continuation of first sheet(1)

The requirement of unity of invention in international application (PCT Rule 13.1) is not satisfied unless there is a technical relationship between a group of inventions as set forth in claims involving one or more of the same or corresponding special technical feature. The term "special technical feature" means a technical feature clearly showing the contribution achieved by the inventions as set forth in the claims as a whole (PCT Rule 13.2). The requirement of unity of invention is judged without considering whether the group of inventions are described in separate claims or in a single claim in the alternative form (PCT Rule 13.3).

In the present case, the inventions relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS:144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO:115,116, 129, 130, 131, 132, 133 and 134 have a matter in common "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells". However, there had been publicly known endothelin-1, monocyte chemotactic protein-1, etc. as "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells", as the applicant recognizes. Therefore, it can be concluded that there is no "special technical feature" common to the inventions relating to the above-described base sequences (or amino acid sequences) as set forth in the claims.

Such being the case, the claims involve 86 separate inventions respectively relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS:144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO:115,116, 129, 130, 131, 132, 133 and 134.

	国際出願番号 ＰＣＴ／ＪＰ００／０６８４０

A. 発明の属する分野の分類（国際特許分類（ＩＰＣ））

Int.Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

B. 調査を行った分野

調査を行った最小限資料（国際特許分類（ＩＰＣ））

Int.Cl⁷ C12N15/11-15/62, C07K14/00-14/825

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース（データベースの名称、調査に使用した用語）

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
BIOSIS (DIALOG), WPI (DIALOG)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO, 99/14327, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、PRO246, FIG.26 (Accession No.X28436), FIG.27 (Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、FIGURE 16 (Accessiion No.X52221),	2, 4, 11, 12, 36-40, 43, 45, 46

[X] C欄の続きにも文献が列挙されている。　　　　[ ] パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー
「A」特に関連のある文献ではなく、一般的技術水準を示すもの
「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献（理由を付す）
「O」口頭による開示、使用、展示等に言及する文献
「P」国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献
「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「&」同一パテントファミリー文献

国際調査を完了した日　　19.12.00	国際調査報告の発送日　**26.12.00**
国際調査機関の名称及びあて先 　日本国特許庁（ISA／JP） 　郵便番号１００－８９１５ 　東京都千代田区霞が関三丁目４番３号	特許庁審査官（権限のある職員）　　4N 8214 　　内 田 俊 生　　[印] 電話番号　０３－３５８１－１１０１　内線　３４８８

様式ＰＣＴ／ＩＳＡ／２１０（第２ページ）（１９９８年７月）

C（続き）.	関連すると認められる文献	
引用文献の カテゴリー＊	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
	FIGURE 17(Accession No. Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.) 24. 8月. 1999 (24. 08. 99) 特に、SEQ ID NO:2(Accession No. X87000), SEQ ID NO:1(Accession No. Y27096) （ファミリーなし）	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.) 18. 11月. 1999 (18. 11. 99) 特に、SEQ ID NO:39(Accession No. Z65278), SEQ ID NO:291(Accession No. Y76303) & AU, 9938831, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.) 2. 3月. 2000 (02. 03. 00) 特に、SEQ ID NO:37(Accession No. A23441), SEQ ID NO:38(Accession No. Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.) 23. 3月. 2000 (23. 03. 00) 特に、FIGURE 15(Accession No. A30052), FIGURE 16(Accession No. Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene ex- pression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Ex- pression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

国際調査報告	国際出願番号 PCT／JP00／06840

第Ⅰ欄　請求の範囲の一部の調査ができないときの意見（第1ページの2の続き）

法第8条第3項（PCT17条(2)(a)）の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. [X] 請求の範囲　22,33,51,57,66,69,76　は、この国際調査機関が調査をすることを要しない対象に係るものである。
つまり、
　　請求の範囲22，33，66，69の発明は「細胞のアポトーシスを抑制、促進または調節する方法」に関するものであるが、明細書にも記載されているように、これらはヒトの体内で治療を目的として実施されるものであるから、これらの発明は人の身体の治療による処置方法に該当する。また、請求の範囲51，57，76の発明は、「抗体と

2. [ ] 請求の範囲　＿＿＿＿＿＿＿＿＿　は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、

3. [ ] 請求の範囲　＿＿＿＿＿＿＿＿＿　は、従属請求の範囲であってPCT規則6.4(a)の第2文及び第3文の規定に従って記載されていない。

第Ⅱ欄　発明の単一性が欠如しているときの意見（第1ページの3の続き）

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

　　国際出願における発明の単一性の要件（PCT規則13．1）は、請求の範囲に記載された一群の発明の間に一又は二以上の同一又は対応する特別な技術的特徴を含む技術的関係があるときに限り、満たされるものであって、この「特別な技術的特徴」とは、請求の範囲に記載された各発明が全体として先行技術に対して行う貢献を明示する技術的特徴のことである（PCT規則13．2）。また、発明の単一性の要件の判断は、一群の発明が別個の請求の範囲に記載されているか単一の請求の範囲に択一的な形式によって記載されているかを考慮することなく行われる（PCT規則13．3）。
　　そこで、請求の範囲をみると、請求の範囲に記載された配列番号143，145，147，149，151，153，155，157，168，170，172，111，113

1. [ ] 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。

2. [ ] 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。

3. [ ] 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。

4. [X] 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

　　請求の範囲中の配列番号143で表される塩基配列又は配列番号144で表されるアミノ酸配列に関連した発明

追加調査手数料の異議の申立てに関する注意
　　[ ] 追加調査手数料の納付と共に出願人から異議申立てがあった。
　　[ ] 追加調査手数料の納付と共に出願人から異議申立てがなかった。

様式PCT／ISA／210（第1ページの続葉（1））（1998年7月）